



US006211431B1

(12) **United States Patent**
Boevink et al.

(10) **Patent No.:** **US 6,211,431 B1**
(45) **Date of Patent:** **Apr. 3, 2001**

(54) **PLANT TRANSCRIPTION REGULATORS FROM CIRCOVIRUS**

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(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

(21) Appl. No.: **08/793,634**

(22) PCT Filed: **Aug. 30, 1995**

(86) PCT No.: **PCT/AU95/00552**

§ 371 Date: **Jun. 9, 1997**

§ 102(e) Date: **Jun. 9, 1997**

(87) PCT Pub. No.: **WO96/06932**

PCT Pub. Date: **May 7, 1996**

(30) **Foreign Application Priority Data**

Aug. 30, 1994 (AU) PM 7770
Nov. 7, 1994 (AU) PM 9281

(51) **Int. Cl.**⁷ **C12N 15/33**; C12N 15/82; C12N 15/90; A01H 5/00

(52) **U.S. Cl.** **800/278**; 435/69.1; 435/320.1; 435/468; 536/24.1; 800/280; 800/288; 800/298; 800/301; 800/302

(58) **Field of Search** 435/69.1, 320.1, 435/410, 419, 468; 536/24.1, 23.72, 23.6; 800/301, 302, 278, 280, 288, 295, 298, 279

(56) **References Cited**

FOREIGN PATENT DOCUMENTS

43 06 832 C1 2/1994 (DE) C12N/15/82

OTHER PUBLICATIONS

Kim et al, *Plant Mol. Biol.*, vol. 24, pp. 105-117, 1994.*
Boevink, et al. (1995) "Sequence of Subterranean Clover Stunt Virus DNA: Affinities with the Geminiviruses", *Virology* 207:354-361.

Boevink, et al. Abstracts of the 9th International Congress of Virology, Aug. 8-13, 1993, Glosgow, Scotland, U.K., P 68-1 "Subterranean Clover Stunt Virus—A Hypervariable DNA Virus".

Chu, et al. (1993) "Replication of Subterranean clover stunt virus in pea and subterranean clover protoplasts", *Virus Res.* 27:173-183.

Chu, et al. (1993) "Putative full-length clones of the genomic DNA segments of subterranean clover stunt virus and identification of the segment coding for the viral coat protein", *Virus Res.* 27:161-171.

Karan, et al. (1994) "Evidence for two groups of banana bunchy top virus isolates", *Journal of General Virology* 75:3541-3546.

Katul, et al. (1995) "Sequence analysis of a faba bean necrotic yellows virus DNA component containing a putative replicase gene", *Journal of General Virology* 76:475-479.

Surin, et al. Abstracts of the 9th International Congress of Virology, Aug. 8-13, 1993, Glosgow, Scotland, U.K., P 62-1, The Subterranean Clover Stunt Virus Genome Consists of Micro-Chromosomes Encoding Single.

Wu, et al. (1994) "Nucleotide Sequences of Two Circular Single-Stranded DNAs Associated with Banana Bunchy top Virus", *Phytopathology* 84(9):952-958.

Xie, et al. (1995) "Molecular Cloning, Sequence Analysis, and Detection of Banana Bunchy Top Virus in Hawaii", *Phytopathology* 85(3):339-347.

* cited by examiner

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(57) **ABSTRACT**

The present invention is directed to transcription regulators and transcription regulator-like sequences of nanovirus origin. As used in the specification, the nanovirus group is considered to include subterranean clover stunt virus (SCSV), cocnut foliar decay virus (CFDV), banana bunchy top virus (BBTV), milk vetch dwarf virus (MDV), and faba bean necrotic yellow virus (FBNYV). The transcription regulators and transcription regulator-like sequences of the instant invention are useful in genetic engineering of plants and in particular leguminous plants such as to facilitate or control expression of foreign genes. The transcription regulators and transcription regulator-like sequences of the present invention are also useful in facilitating different levels of expression in different plant tissue types.

38 Claims, 45 Drawing Sheets

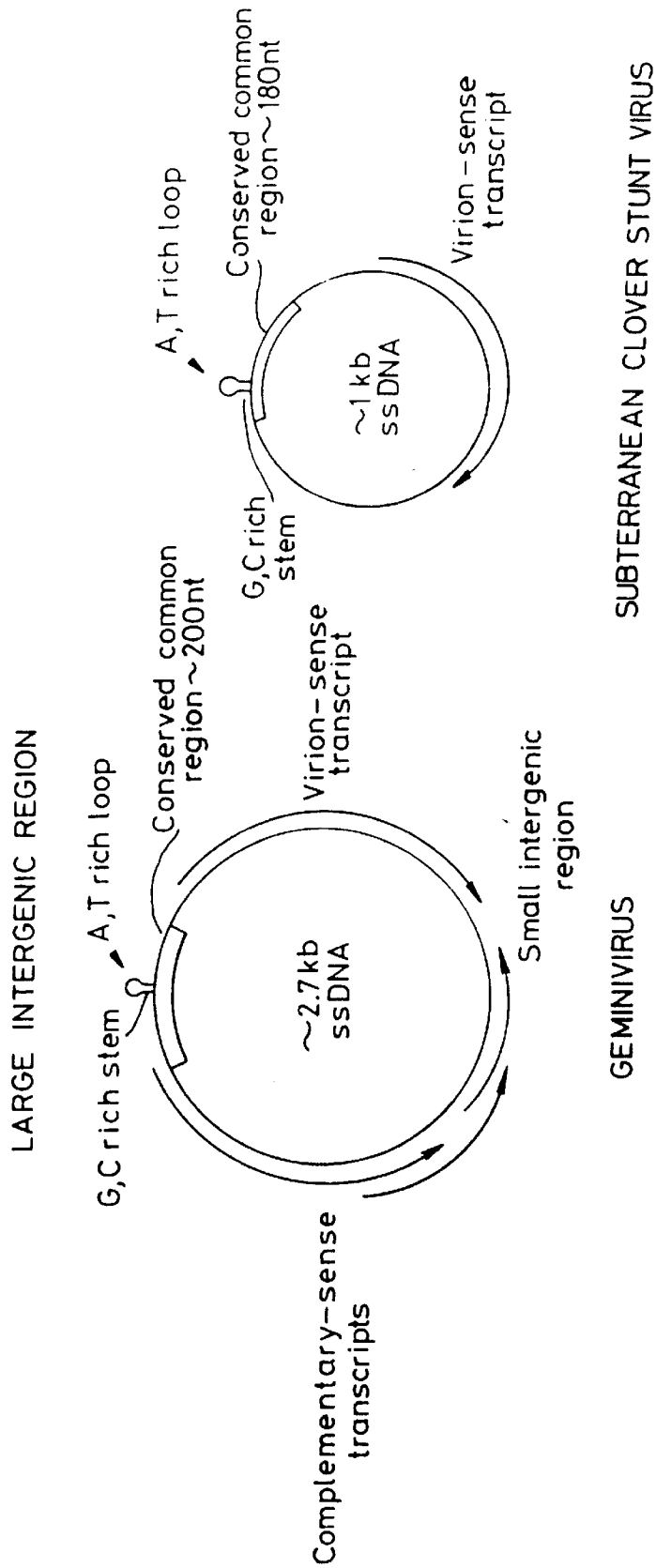
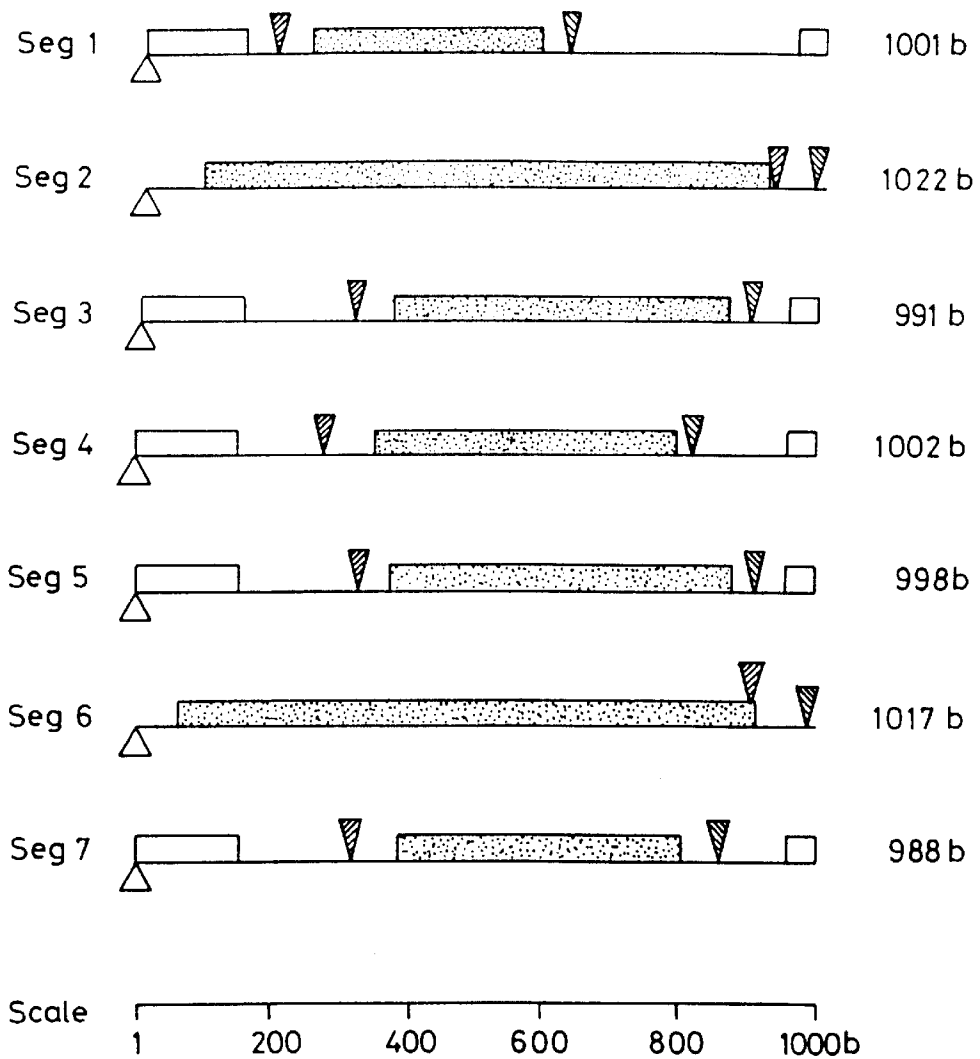


Fig. 1



LEGENDS	△ Stem-loop	▽ TATA box	▽ Polyadenylation and termination signal
	□ Common region	▨ ORF	

Fig. 2

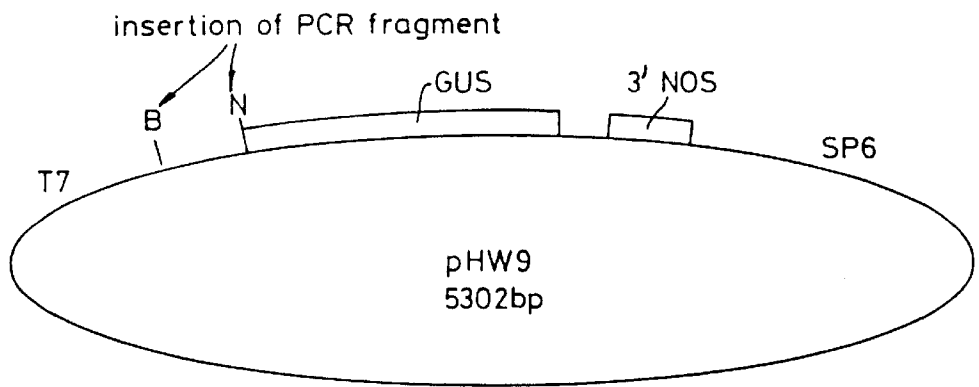
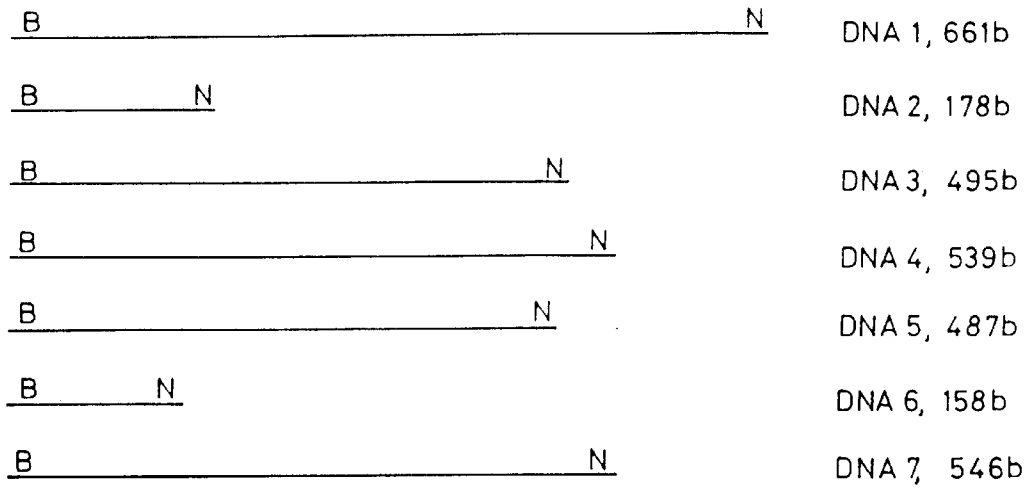
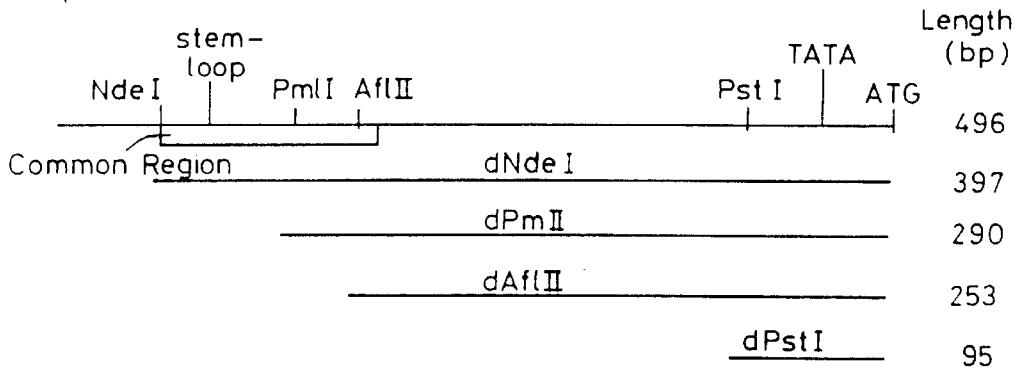


Fig. 3

Component 5 non-coding region and deletions.



Component 7 non-coding region and deletion

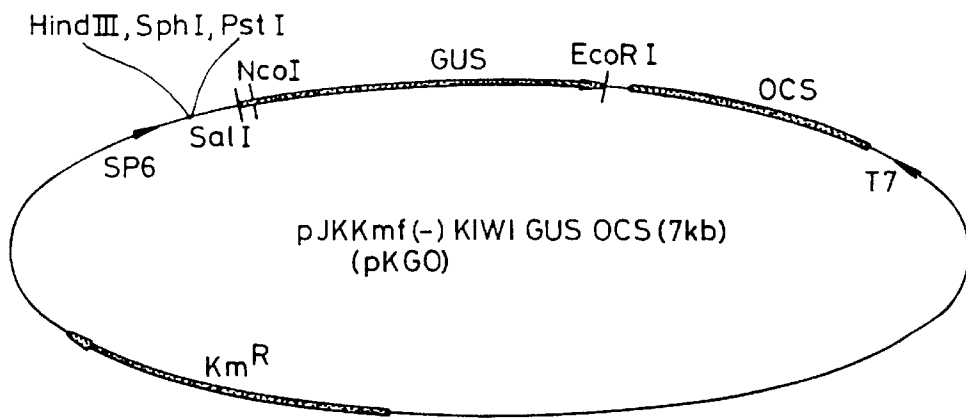
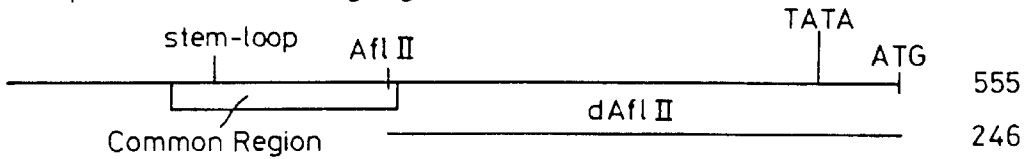


Fig.4

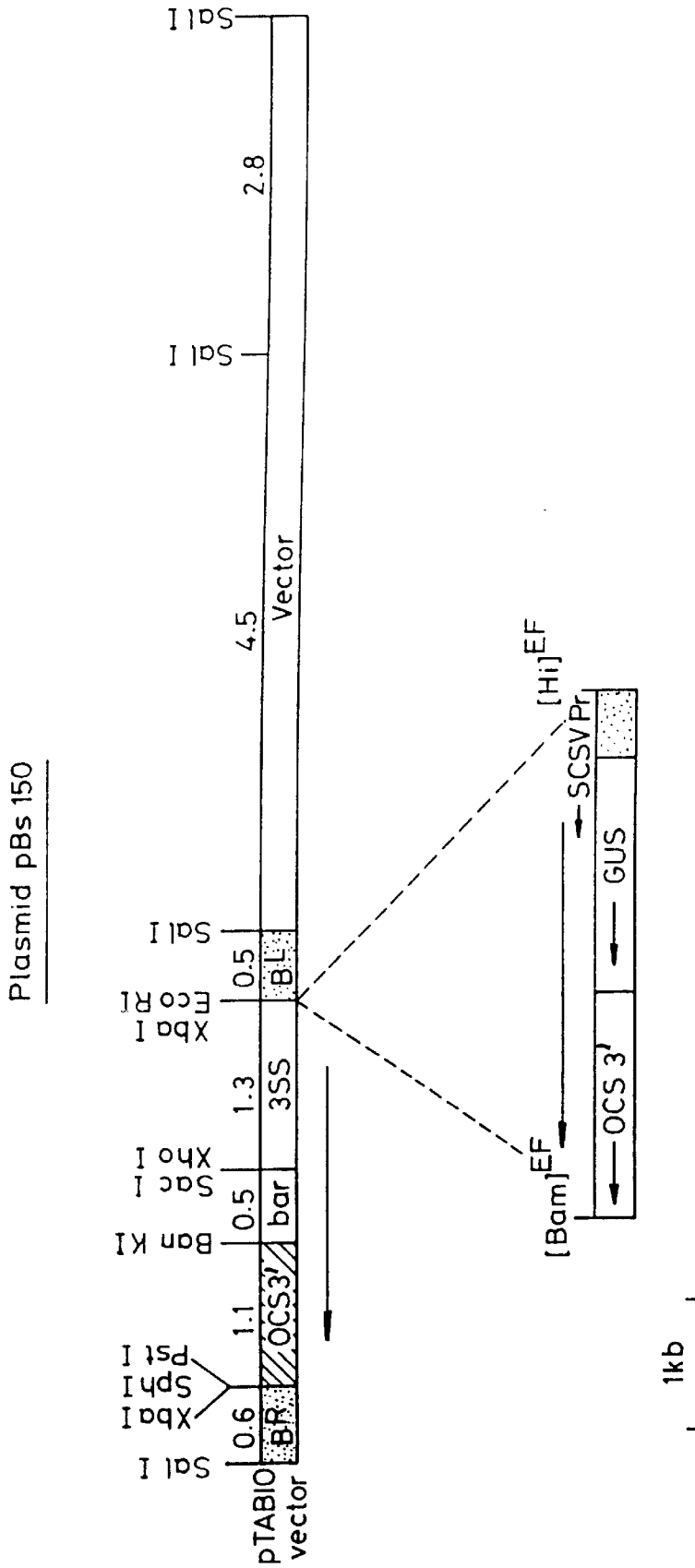


Fig. 5

COMPONENT 1

1	TAGTATTACC	CCCGTGCCGG	GATCAGAGAC
61	CCTTGGATTA	AATGACACGT	GGACGCTCAG
121	GAACGAATCT	GACGGAAGAG	CGTTCACACT
181	GTCTTGGGTC	TATAAATAGA	GTGCTTCTGA
241	GATTCTGGTG	ATGGTTACAA	TACATACTCA
301	GAAGTTTTAT	ATAAAATAGG	TATTATTATG
361	GTTTTAATTA	TATTATGTTG	TGCTGTTTCCT
421	TTATCTTCGT	CTTCTATTAT	GAAGAGGAAG
481	GAAGAAACTG	GTCCTCATCG	TGAAAGAAGA
541	CAGAATAATA	ATGATAATGT	AAATAGATTT
601	ATGAGAATTA	TTATTATTCT	GTTCTTCGTC
661	TGGCGTCTGG	AGAGAGAAAG	GAATAATTGT
721	TGTCTTTACT	TCGCCTCGAA	GAAAGACACA
781	GAAGCTTCCT	CGAAGCAGCG	TATAACTTTA
841	ATTGCGGCTG	TAAACGTGTC	AAGTTGTGAG
901	ATTGTTTTAA	TTTAATTCCG	CGAAGCGATA
961	GATGACGTCA	TATGTCTCCG	TGCCTACGTC

Fig. 6(i)

COMPONENT 1 (cont.)

ATTTGACCAA TAGTTGACTA GTATAATAGC	60
GATCTGTGAT GCTAGTGAAG CGCTTAAGCT	120
TAGATCTAGT TAGCGTACTT AGTACGCGTT	180
ACAGATTGTT CAGAATTTCA TAGCGAGATG	240
TATGAAGAAG GTGCTGGAGA TGCGAAGAAG	300
TTATGTATTG TAGGGATTGT AGTTTTATGG	360
CGCTATGCTA AATCAACGAT GGACGCTTGG	420
ATGGCTTCAA GGATTACTGG TACTCCGTTT	480
TGGGCTGAAA GAAGAACTGA AGCGACGAAC	540
AGTTGATATG TTGTAATTTT ATATGGATTA	600
TGTGTTTTTT AAGCTTTTTC TGTGTTTTAA	660
AAGGTAGACG ACGATGTAGT GGATTACAGT	720
TTTCAAGTTG TGAGTGTTAT TGCTTTTGAG	780
ATTTGAATTT GGTTTTGGCG CGTTAGTGAA	840
TGGCTGAAAT AAGATAATAG ATATATTATT	900
TGTTAAGTGA TAAATGAAAC GAAGCGTTTT	960
AGCACGGGGC T	1001

Fig. 6(ii)

COMPONENT 2

1 TAGTATTACC CGACCTTGCC ACACCTCCTT
61 ACTTTCTCTC TCTAAGCTTA TATGGCTAGA
121 GAGATAGAGA GAGAAACATT CCTCTCCCTC
181 GTCGGCGACG AACTGCAAC TACTGGACAG
241 AACAAAATTC GTCTTGGTGG ATTGAAGAAG
301 GCGAGAGGCA GCGATTCTCA GAATCGCGAT
361 ATTGGGATTC CGGTCATGAA GGGTTCGAAC
421 GATCCCGAAG AAATGCAATT GAAGGATCCA
481 TTGAAAGAGG AATATTGTTC CTGTTATGAT
541 CTTCACGAGG ATTTAATGGC GGAACCAGAT
601 GACGGAGGAG AAGGAAAGAC GAGCTTCGCG
661 ACAGCCGGAG GGAAGACCCA GGACGTATTA
721 ATTGCGTTTG ATGTTCCCAG GTGTTCTTCG
781 TTGAAGAACA GAGTTTTTGC AAGTACAAAA
841 TTAGTTCATT TAATTGTGTT TGCCAACGTG
901 AACTTGTA TATCAATTG TTGAATAAAA
961 GCGAAGCGGT AGCCGGTCAT AACACTGTTG
1021 CT

Fig. 6(iii)

COMPONENT 2 (cont.)

GGAACACTTT	CTCTCTCTAG	AAAGTGTGAG	60
AGGTACTGTT	TTACATTAAA	TTACGCTACT	120
TTCTCTCAAG	ACGAATTAAA	CTATTTTCGTT	180
AAACACCTCC	AGGGATTTGT	ATCGTTCAAG	240
AAATTTGGTA	ATCGAGCTCA	CTGGGAAATT	300
TATTGCTGTA	AAGAAACCCT	AATTTCTGAA	360
AAGCGGAAGA	CGATGGAGAT	TTATGAAGAG	420
GATACTGCTC	TTCGATGTAA	GGCGAAGAAA	480
TTTCAGAAAC	TCCGTCCATG	GCAAATTGAG	540
AAGGAATTAA	TCAGGTATGG	ATGGTTTTAT	660
TATATGTATG	CTCAAGACCC	AGAGAGGAAT	720
GAGATGATGA	ACTATCAGGC	GATGGAGATG	780
TATAGGCCTG	TAGATCTTTG	TATTAGGAAG	840
GCACCTGACC	CCACGCGCAT	AAGTGAGGAC	900
GAATATATAT	TATTGTTTTA	ATTTAATTCC	960
CCCTTGGAAC	ACTATATATA	GCAAGGTCGG	1020
			1022

Fig. 6(iv)

COMPONENT 3

1 TAGTATTACC CCCGTGCCGG GATCAGAGAC
61 CCCTTGGATT AGATGACACG TGGACGCTCA
121 TGAACGAATC TGACGGAAGA GCGGACATAC
181 TGTATCTCTT TACAGCTATA TTGATGTGAC
241 GTAGGAAATT GCTCGCTAAG TTATTCTTTT
301 ATTAAATGAG TGGCTATAAA TAGATGTTTC
361 TCTTGTGTTA ATGGCGTTAA GGTATTTCTC
←
421 TATGAACGAG CACTTGAAGG AAATTAAGAA
481 TGCGTGTGCT GTGTTCGAAG GTTTAACAAA
541 ACGCTTCTCT GGGTTTCTGG AAGGTCTGTC
601 GTGTTTAGTT AGATGGAAGA AGAGCGTTGC
661 GATGCATTAC AAGCTTTATG GATTTGCAGA
721 GTTTCCTAAT TACGGTGAAG ACGATGTAGC
781 GCAATTAGAA GTTGTATTTG ATGATTTAGG
841 AGGTTCTATT AAGATAGAAT TATGAGATGT
→
901 TATTCTTTGA ATTACTCCGC GAAGCGGTGT
961 ATATGTCTCG CCGACAGGCT GGCACGGGGC

Fig. 6(v)

COMPONENT 3 (cont.)

ATTTGACCAA TAGTTGACTA TGAATAATAG	60
GGATCTGTGA TGCTAGTGAA GCGCTTAAGC	120
GCACATGGAT TATGGCCCAC ATGTCTAAAG	180
GTAAGATGCT TTA CTTCGCC TCGAAGTAAA	240
CTGAAAGAAA TTAATTTAAT TCTAAATTAA	300
GTCTTCGTTG TTTTACAACG <u>AAGCTTAGAA</u>	360
TCATCTTCCT GAAGA ACTGA AGGAGAAGAT	420
GAAGGAATTT CTAGAGAATG TAATTAAAGC	480
GAAGGAGTCT GTTGAAGAAG ACGACATACT	540
TGCATATTAT GCAGAGGCCG CGAAGAAGAA	600
AATAAATCTG AAATGGAGAG TTATGGAGGA	660
CATGGAAGAT TTATATTATT CAGAGTTAGG	720
TTATCACGAT GGTGCAATTG TAAATTGTAA	780
TATTGAGTTT ATGTCTATTG TAATTGATAG	840
AATTGTGATT AATGAATAAA GAGTTGTTAT	900
<u>GTTATGTTTT</u> TGTTGGAGAC ATATGACGTC	960
T	991

Fig. 6(vi)

COMPONENT 4

1 TAGTATTACC CCGTGCCGGG ATCAGAGACA
61 CCTTGGATTA GATGACACGT GGACGCTCAG
121 GAACGAATCT GACGGAAGAG CGGACAAACG
181 AGAAGTGAAT GACAGCTGTC TTTGCTTCAA
241 AAGAATAAGC GTACTCAGTA CGCTTCGTGG
301 GTTGTATCAT CAACGAAGAA GTTAAGCTTT ←
361 CAGTGCGCTT AAGACATGTA CTCATGTCTG
421 ACAGGATTTTCT TCTGTTGTG ATAGTATGCG
481 GTTAGTTAGT TGTTTTGTAA GTTTTACTGG
541 AGGTCAAGTT CAGTTGGGTA TGCAGCAAGA
601 TCCTATTGGG GGTTATTTGT ATCATGATGA
661 CAATCTGGAC ATCGAGTCAG ATTATCTGAA
721 AATTAATATT GTAAATGATA AAGGATTAGA
781 TCATACGATG CGTATTAAGG TGTAATTGTT →
841 GTGTTATTTG GTAATTTATG CTTATAAGTA
901 TAATGAGGAT AATAATTGAA TTTGATTAAA
961 TGAGAGTCAC GTGATGTCTC CGCGACAGGC

Fig. 6(vii)

COMPONENT 4 (cont.)

TTTGACTAAA	TGTTGACTTG	GAATAATAGC	60
GATCTGTGAT	GCTAGTGAAG	CGCTTAAGCT	120
CACATGGACT	ATGGCCCACT	GCTTTATTAA	180
GACGAAGTAA	AGAATAGTGG	AAAACGCGTA	240
CTTTATAAAT	AGTGCTTCGT	CTTATTCTTC	300
GTTCTGCGTT	TTAATGGCGG	ACTGGTTTCA	360
←			
TGATTTTTCA	GATATTAAGG	CGTCTTCACA	420
AGGTAAATTA	TCTGAACCTA	GGAAGGTGTT	480
TAGTTTTTAT	GGAAGTAATA	GGAATGTTAG	540
TGATGGCGTT	GTTCGTCCAA	TAGGATATAT	600
TTATGGATAT	TATCAAGGAG	AGAAGACGTT	660
GCCTGATGAA	GATTTTTGGA	AGAGATTTAC	720
TGATAGGTGT	GATGTAAAAT	GTTATGTAGT	780
ATTATCAATA	AAAGAATTTT	TATTGTTATT	840
→			
ATTCTATGAT	TAATTGTGAA	TTAATAAGAC	900
TTAACTCTGC	GAAGCTATAT	GTCTTTCACG	960
TGGCACGGGG	CT		1002

Fig. 6(viii)

COMPONENT 5

1 TAGTATTACC CCGTGCCGGG GTCAGAGACA
61 CCTTGGATTA GATGACACGT GGACGCTCAG
121 GAACGAATCT GACGGAAGAG CGTCATGGTC
181 GTATTGATTT GACTTTACGC GCTTTACTTT
241 TTTGCTCGCG ACGAAGCAAA GTGATTGTAG
301 AACACGGTTT GATTGTGGGT ATAAATATGT
361 ACGAAGATGG TTGCTGTTCG ATGGGGAAGA
421 TCGCGAATTG CTTACAAACC TCCTTCGTCT
481 AATAAGAGAG ATGTTACTGG AGCGGAGGTT
541 ATGAAGAAGG TAATGTTGAT TGCAACATTA
601 CTTATTGTGA AGAGTAATTC GCCTATTGCG
661 TTGATGGTGA AAGAGTCTGT TCAAGATACA
721 TCTTCTGGTA CTGCTGGTAA AGATGTA ACT
781 TCAGGTATTA GTCAGACCCA GCATTTGTAT
841 ATCACACTGG AGACGAGAAT GTATATTGAT
901 TTGTTTTTAT TCTTTGAATT ACTCCGCGAA
961 TGACGTCATA TGTCTCCGCG ACAGGCTGGC

Fig. 6(ix)

COMPONENT 5 (cont.)

TTTGA	CTAAA	TATTG	ACTTG	GAATA	ATAGC	60	
GATCT	GTGAT	GCTAG	TGAAG	CGCTT	AAGCT	120	
CACAT	GTCTA	AAGAATA	AATG	CTTTAC	AGCT	180	
AATTG	CTTTA	AGTAA	AGTAA	GATGCT	TTTAC	240	
CTGCAG	AAAT	TGATG	CTTTA	ATTACC	GGGT	300	
TCTGT	TCGTT	TTCTT	CGTTG	TCATTTT	TACA	360	
AAGGG	TCTGA	GGTCT	CAAAG	GAGAAA	AATAT	420	
AAGGT	TGTAA	GTCAT	GTGGA	GTCTG	TTCTG	480	
AAGCC	ATTCG	CTGAT	GGTTC	AAGGT	ATAGT	540	
ACTAT	GGCTC	CTGGAG	AATT	AGTTA	AATTAT	600	
AATTG	GAGTT	CGTCT	TTTCAG	TAATC	CCTTCG	660	
GTTAC	GATTG	TTGGAG	GAGG	AAAGC	TTGAG	720	
AAGTC	TTTTA	GGAAG	TTTGT	TAAGC	TGGGT	780	
TTAAT	TATTT	ATTCC	AGTGA	TGCGAT	GGAAG	840	
GTATA	AATTGT	GATGAT	TAAT	GAATA	AAGAG	900	
GCGGT	GTGTT	ATGTT	TTTTT	GT	TGGAG	ACATA	960
ACGGG	GCT					998	

Fig. 6(x)

COMPONENT 6

1 CAGTATTACC GCACCTCGCT TACCCTCCTC ←
61 AAAGCACTAG TTGGGTGTTC ACACTTAACT
121 ATGAAAGCGT TCAGTACGCT TGTTGGCAGC
181 GATTTATACA ATTTAAATCC CGCAACACTA
241 GACTGAATCC TCATCTGGAA ATTGCTAGGG
301 AGGAAGATAG TAGAGTAGCT GGTCCCTGGG
361 ATAAGCGTAA GCTGATGGAG AGATTTGAAG
421 CCTCTCTCTA TAGGCGTTGT CTATCAAGGA
481 AGTGGAATTA TGACTTACGC CCTTGGCAAG
541 CAGATTATAG AACGATAATC TGGGTGTATG
601 TTGCAAGACA TCTGTCATTG AAAGATGGTT
661 ATATGATGCA TCTTGTGACT GCTGAGCCTA
721 TTAGTTCAGA GTATGTGAAT TATGGTGTA
781 AACTAAGTA TGAGCCATGT GTAATGCGGG
841 TTGCAAATGT ACTCCCAGAT TTGGGAAAAT
901 GTTGAAAACCT CTGCGAAGGC → AGAAGTTATA
961 TCGGGTAGTT CGCGAAACAG GGTGAGGGAA

Fig. 6(xi)

COMPONENT 6 (cont.)

GCTTCCCTGG	GCCCACTATG	CCTACTAGAC	60
←			
TTGAGGGCGA	AATTCCTATT	TTGCCCTTTA	120
ATGAGAGAGT	GGGACACGAT	CATTTACAGG	180
CATTGCGTCA	GGCTAAGTAT	ATTTTTAATG	240
ATGTAGAGAA	GGCGCAATTG	TACGCGATGA	300
AGTATGGGTT	GTTTATTAAG	AGAGGATCGC	360
AAGATGGAGA	AGAGATGAAA	ATTGCTGATC	420
AGATGGCTGA	AGAACAACGT	TGTTCTTCTG	480
AAGAAGTGAT	GCATTTGTTA	GAGGAAGAAC	540
GACCTGCTGG	TAATGAAGGC	AAATCTACAT	600
GGGGTTATCT	GCCTGGAGGA	AAGACACAAG	660
AGAATAATTG	GGTATTTGAC	ATACCCAGAG	720
TAGAACAGGT	TAAGAATAGG	GTAATGGTGA	780
ATGATAATCA	TCCTGTTCAT	GTAATTGTGT	840
TAAGTGAAGA	TAGAATAAAA	TTAATTCGTT	900
AAAAAAATGT	GTTTTGAGAG	AAGTCCCACA	960
GCGAGCAATA	TAAGGCGAGG	TGCGTAT	1017

Fig. 6(xii)

COMPONENT 7

1 TAGTATTACC CCGTGCCGGG ATCAGAGACA
61 CCTTGGATTA GATGACACGT GGACGCTCAG
121 GAACGAATCT GACGGAAGAG CGGACATACG
181 GTATCTCTTT ACAGCTATAT TGATGTGACG
241 TAGGAAATTG CTCGCTAAGT TATTCTTTTC
301 TAAATGAGTG GCTATAAATA GTGTCGATGC
361 CTGTTCTGGT TTTAAGCGAT GGTCAGTTTT
←
421 GATGTTCTTG TAAGCGATAG CAGAAGAAGT
481 GTGATTAACG TGAAGGTACT GAGGTTGATT
541 AAGGTTATGT TTCGTCTGTG TTACAGATAC
601 TGTAAGATGG AGCTATGGAC TTCGTTGAAG
661 TTGCAGAGGA AGCTTAATGG TATATGTGTT
721 GTAAGTAATG TTAAAGAGTT GATTAATAGA
781 AATCCTATAT GTTGTTTGTA TCATATGGAC
841 TATGAGATAA GAGTTGTTAT TAATGCTTAT
901 TTTTATTCGC GAAGCGGTGT GTTATGTTTT

Fig. 6(xiii)

COMPONENT 7 (cont.)

TTTGACTAAA	TATTGACTTG	GAATAATAGC	60
GATCTGTGAT	GCTAGTGAAG	CGCTTAAGCT	120
CACATGGATT	ATGGCCCACA	TGTCTAAAGT	180
TAAGATGCTT	TACTTCGCTT	CGAAGTAAAG	240
TGAAAGAAAT	TAATTTAATT	CTAATTAAT	300
TGCCTCACAT	CGTATTCTTC	TTCGCATCGT	360
AGTTTTCCCTG	AGATATACGA	TGTGAGCGAC	420
GTAGCTGTTG	AGGTCGAAGA	GAAGGTTCAA	480
GAAGCTGTTG	ATGAAGATAG	AGTTGGAGTG	540
AGACGAGAAC	TGAAGATTAC	GTTGTTGGGT	600
TCTTCAGGCA	AGTATTCAGT	TCAATCTTTG	660
AGTAATTACT	GTATAGGTAT	TGATATGTTT	720
TGTAAATGGA	TTACATCTGT	TCAAGGTGTT	780
GAAGAGTAAT	TAATAGTAAT	TATGATTAAT	840
GAGGAATAAA	GAATGATTAA	TATTGTTTAA	900
TGTTGGAGAC	ATCACGTGAC	TCTCACGTGA	960
TGTCTCCGCG	ACAGGCTGGC	ACGGGGCT	988

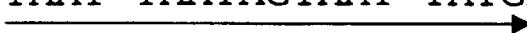
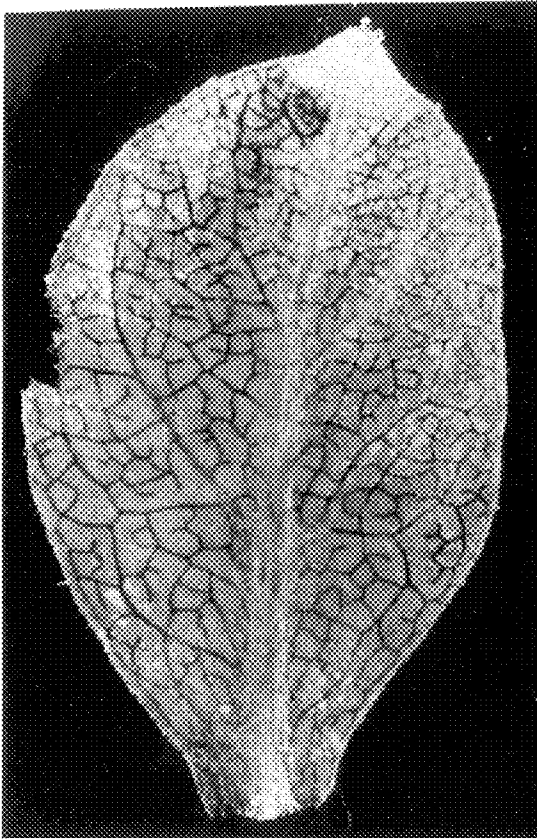


Fig. 6(xiv)

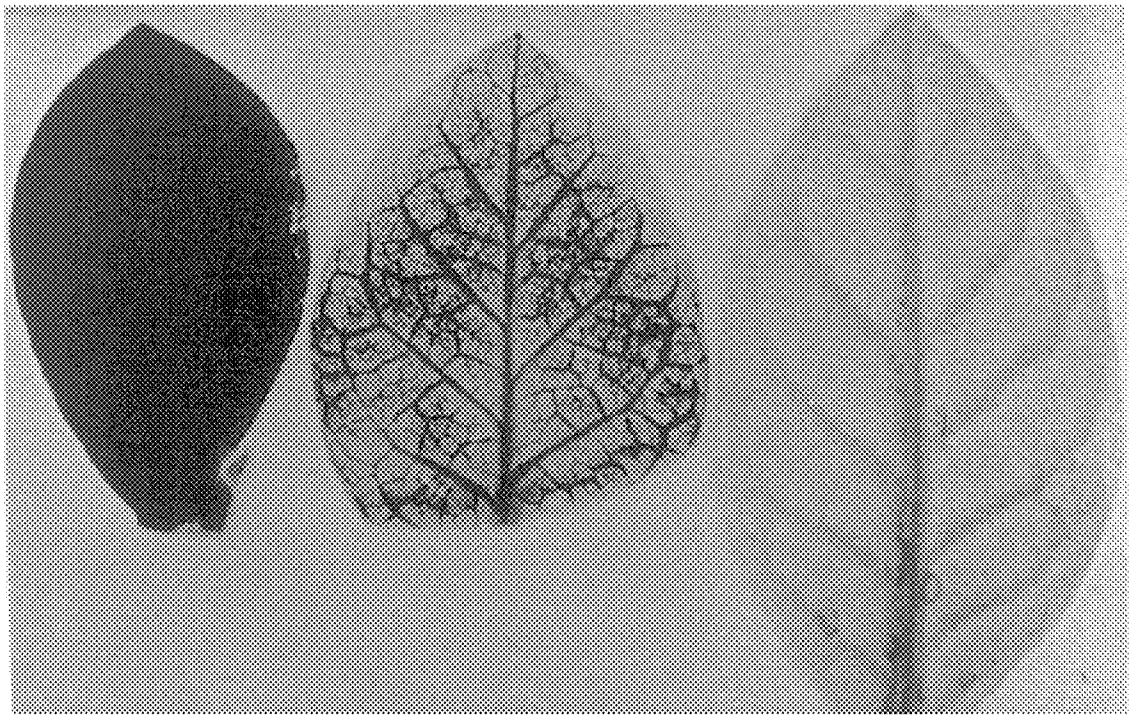


Tobacco



Subterranean Clover

Fig. 7



S4nc

S5nc

NT

Fig. 8a

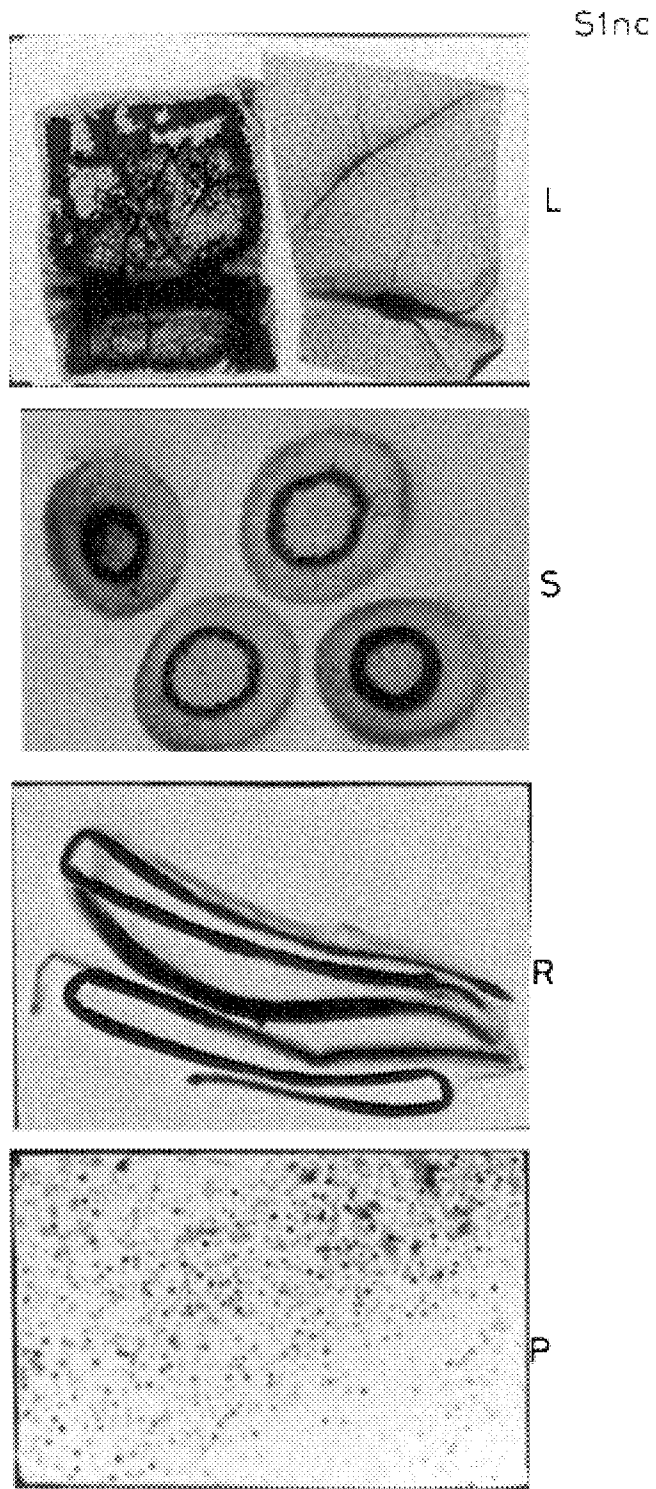


Fig. 8b

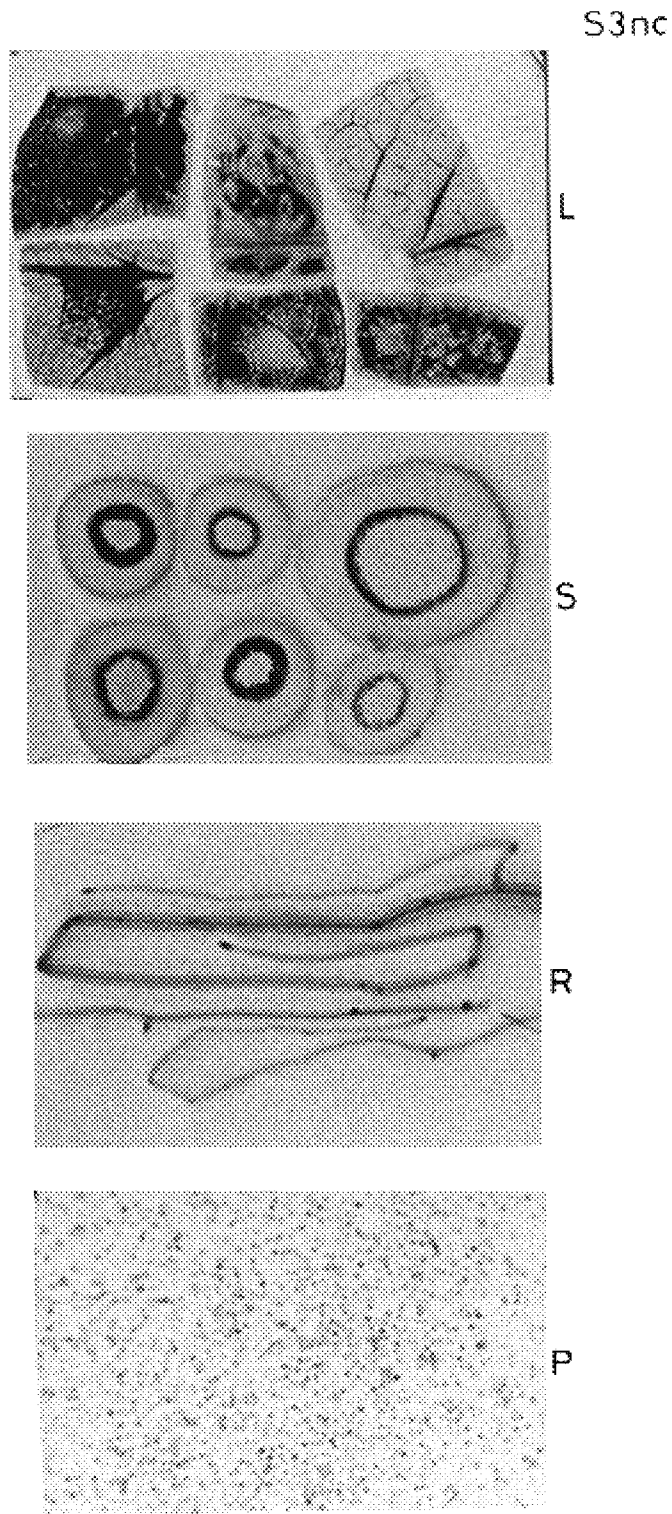


Fig. 8c

S4nc

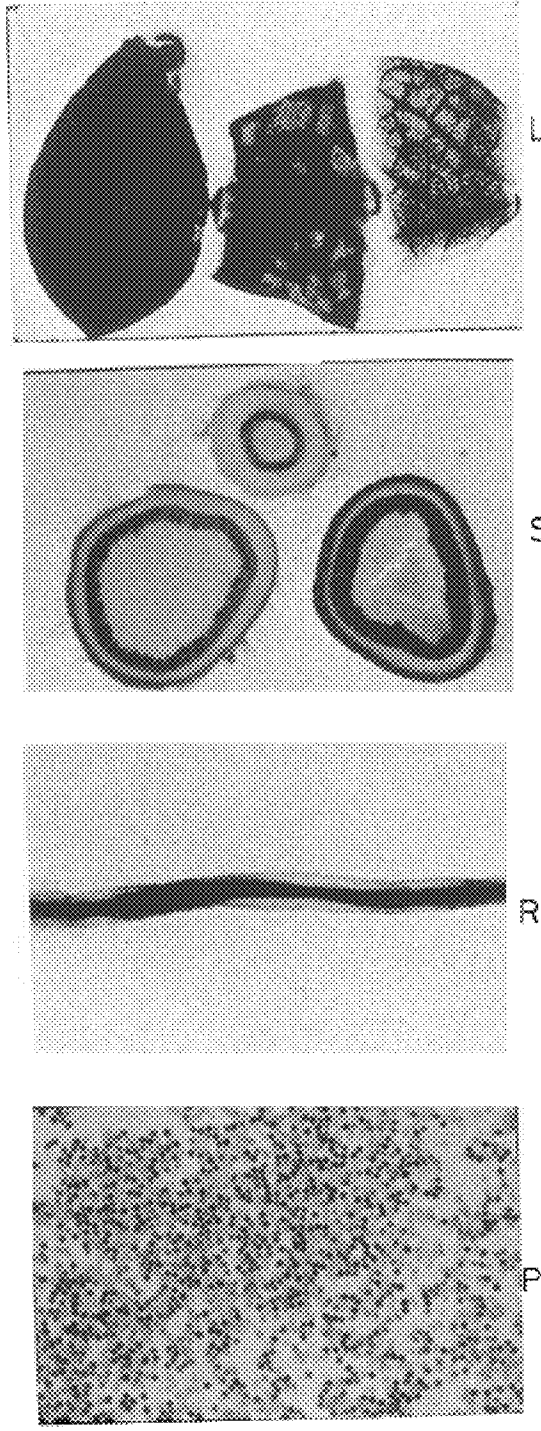


Fig. 8d

S5nc

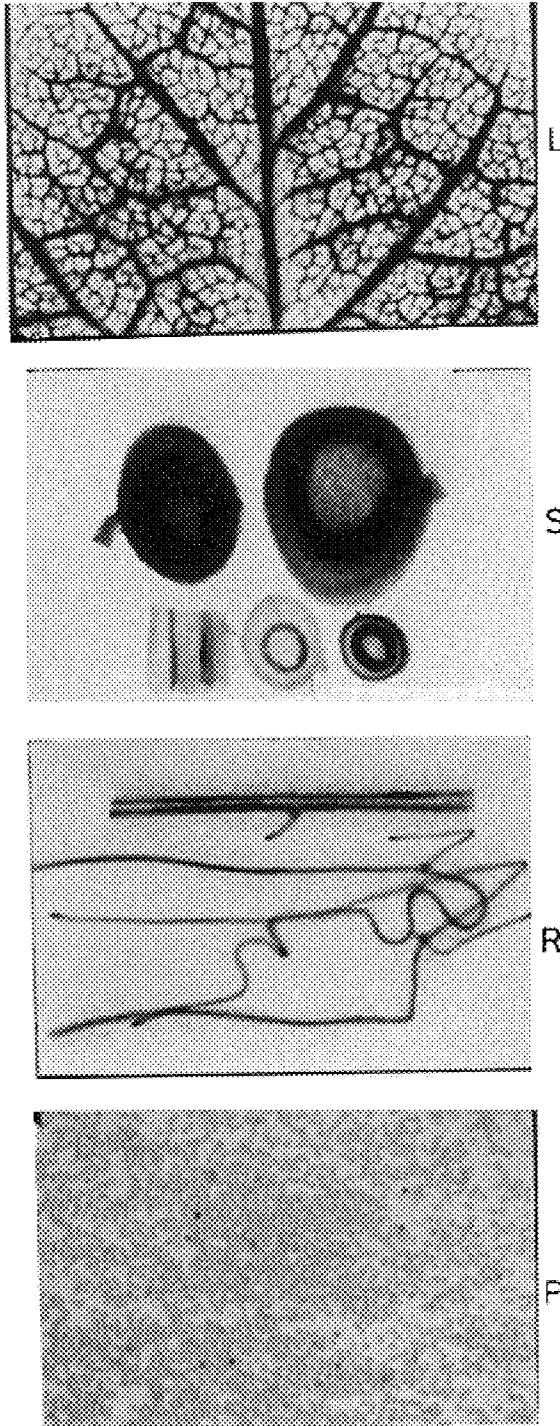
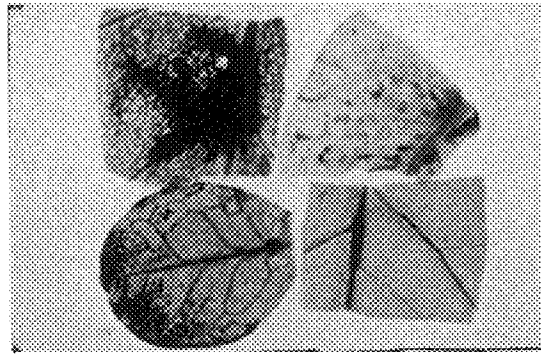
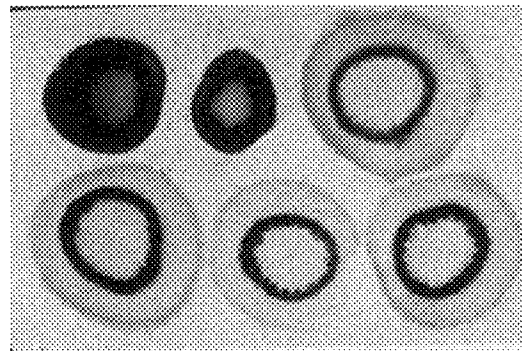


Fig. 8e

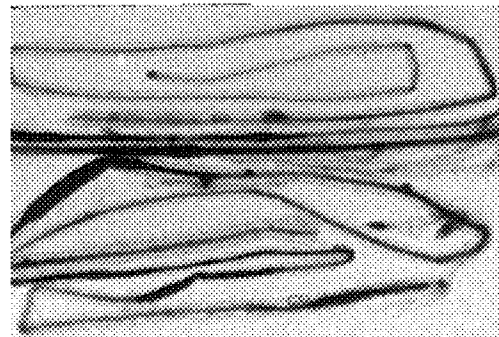
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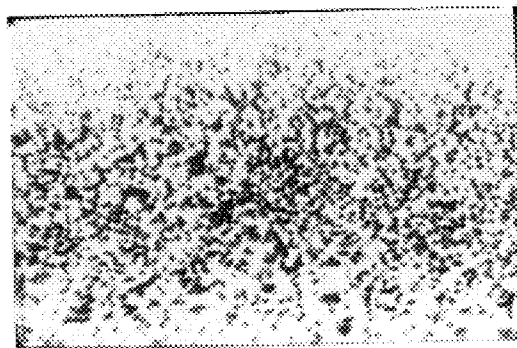
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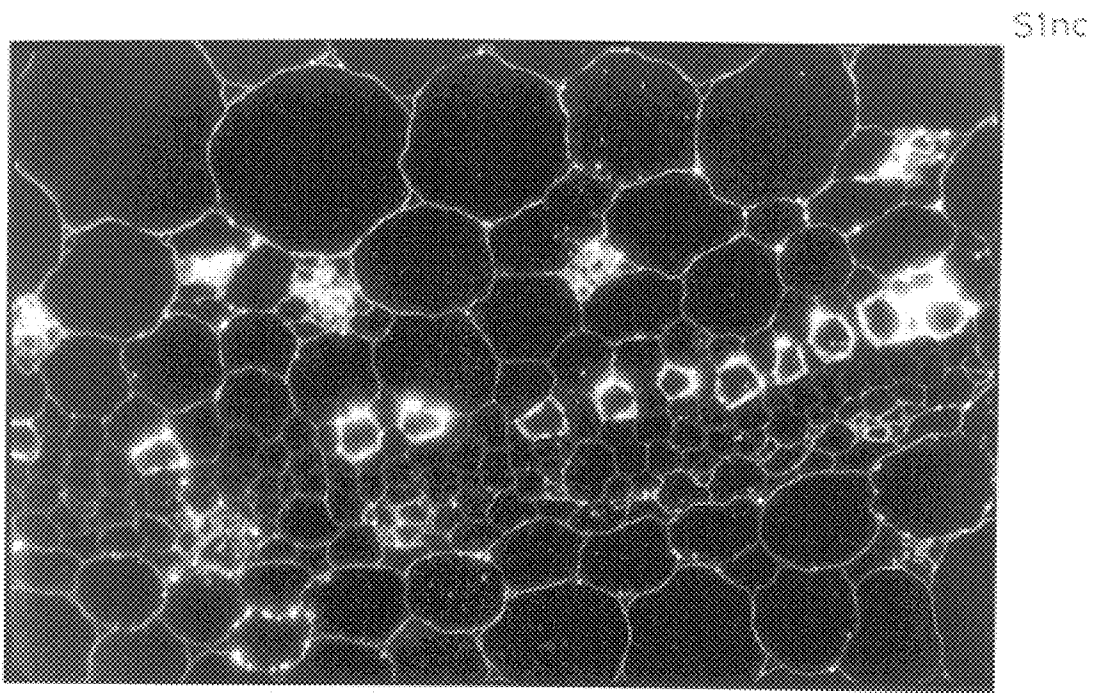


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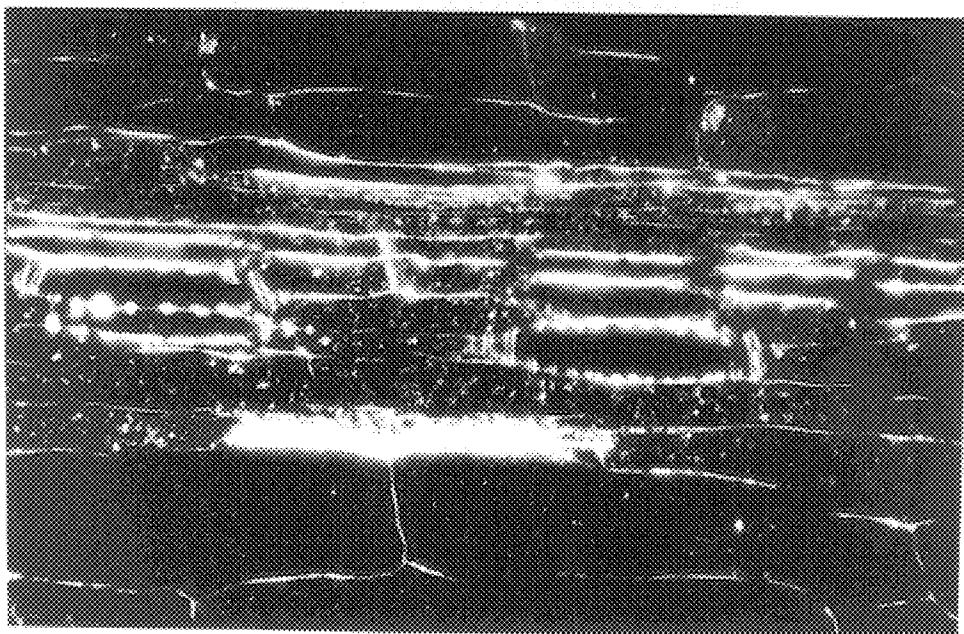
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Fig.8f



S1nc

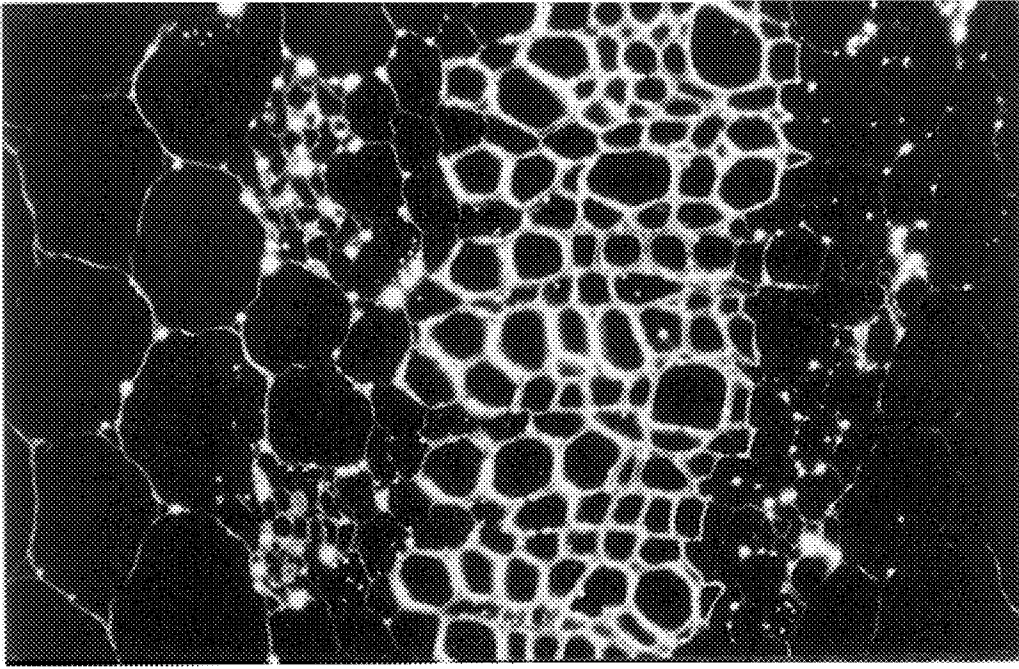
T



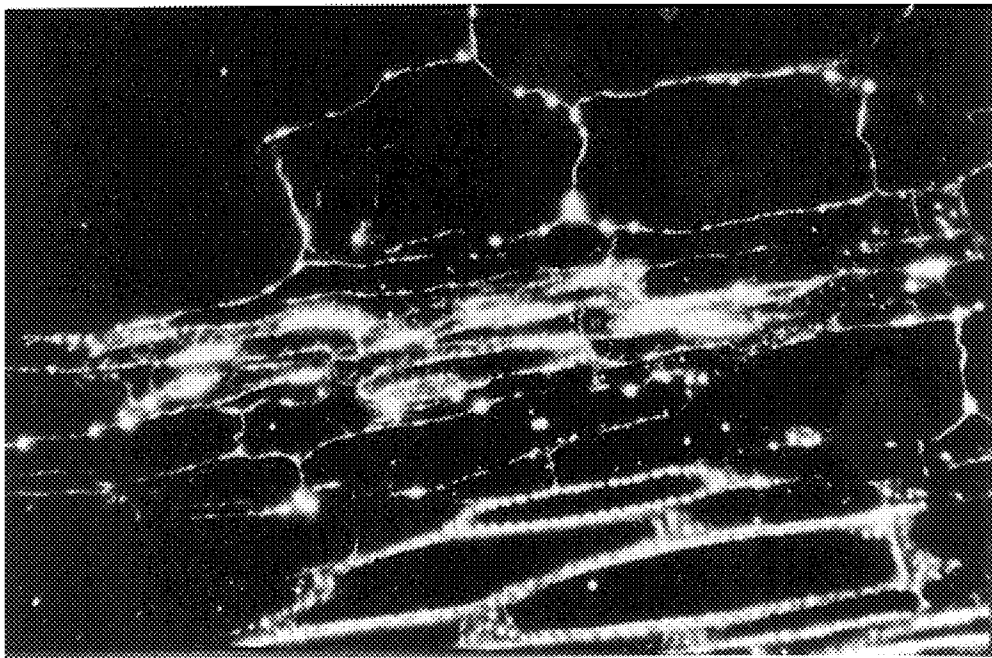
L

Fig. 9a

S3nc



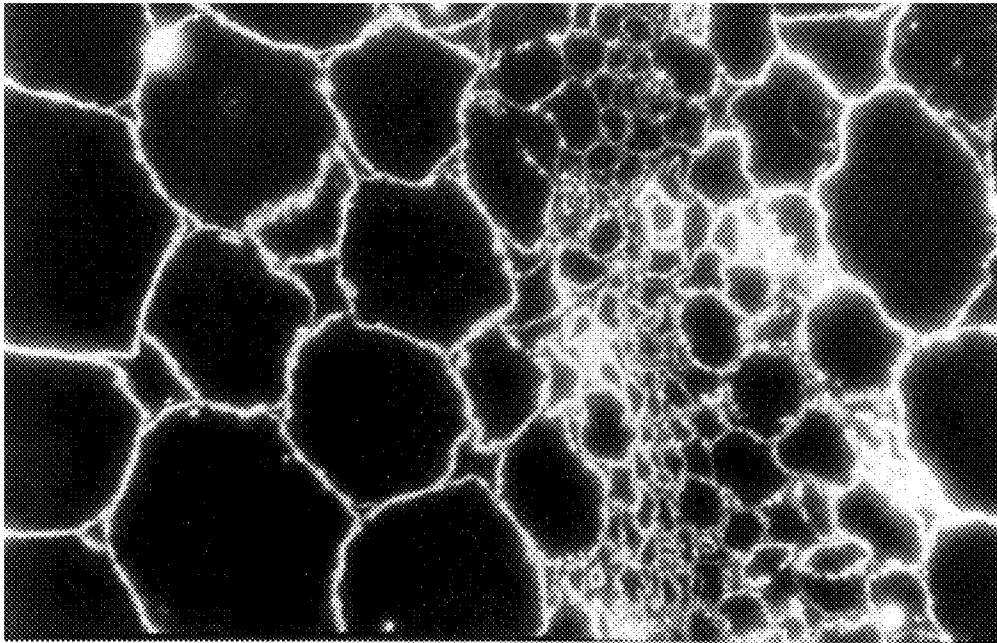
T



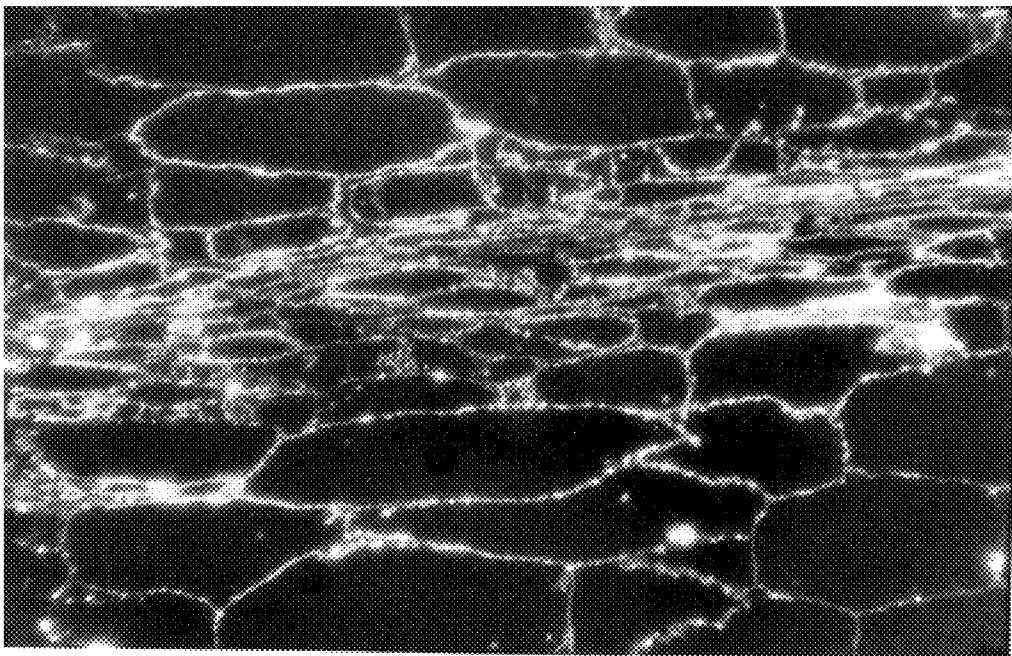
L

Fig. 9b

S4nc



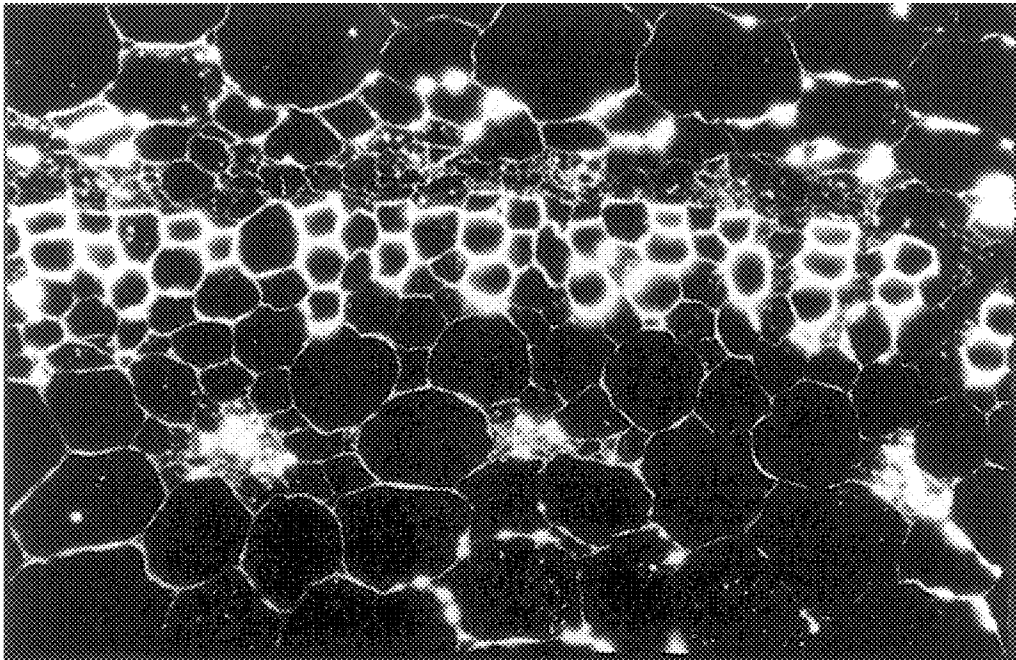
T



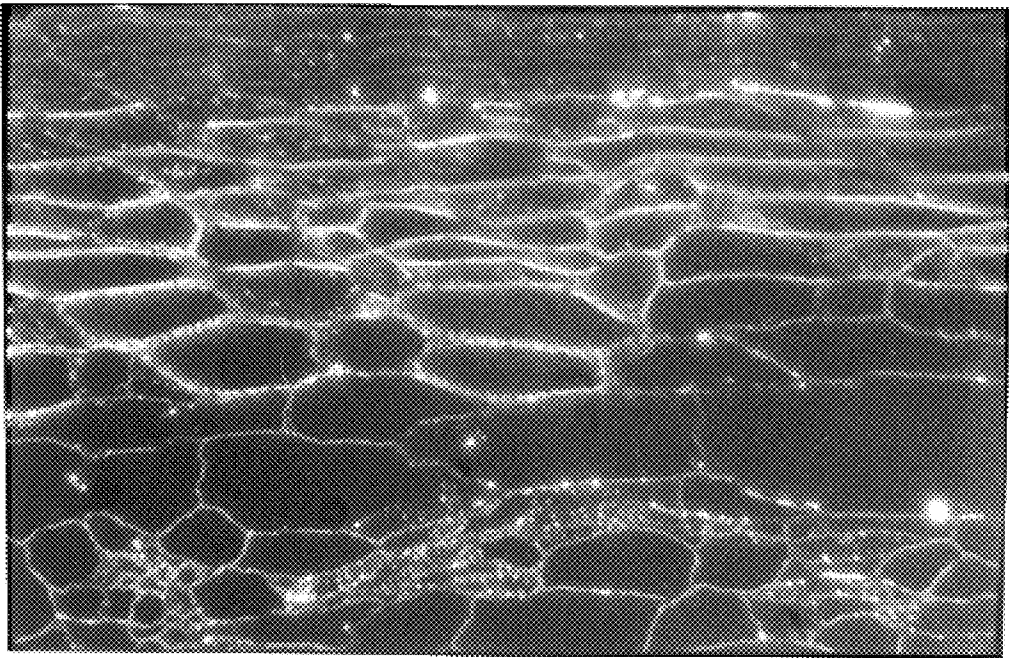
L

Fig. 9c

S5nc



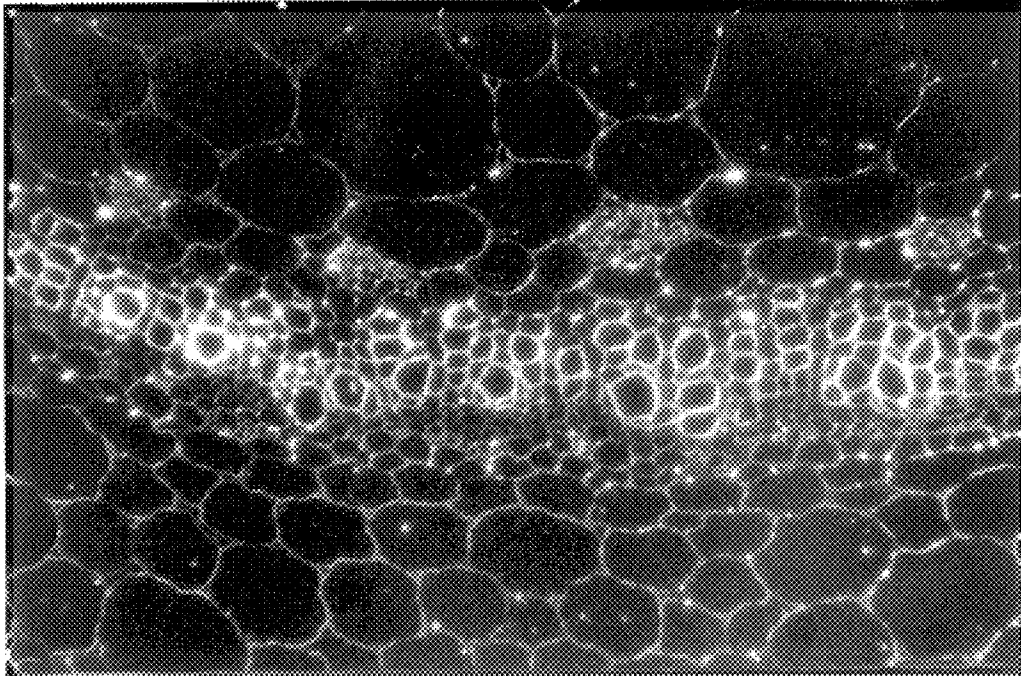
T



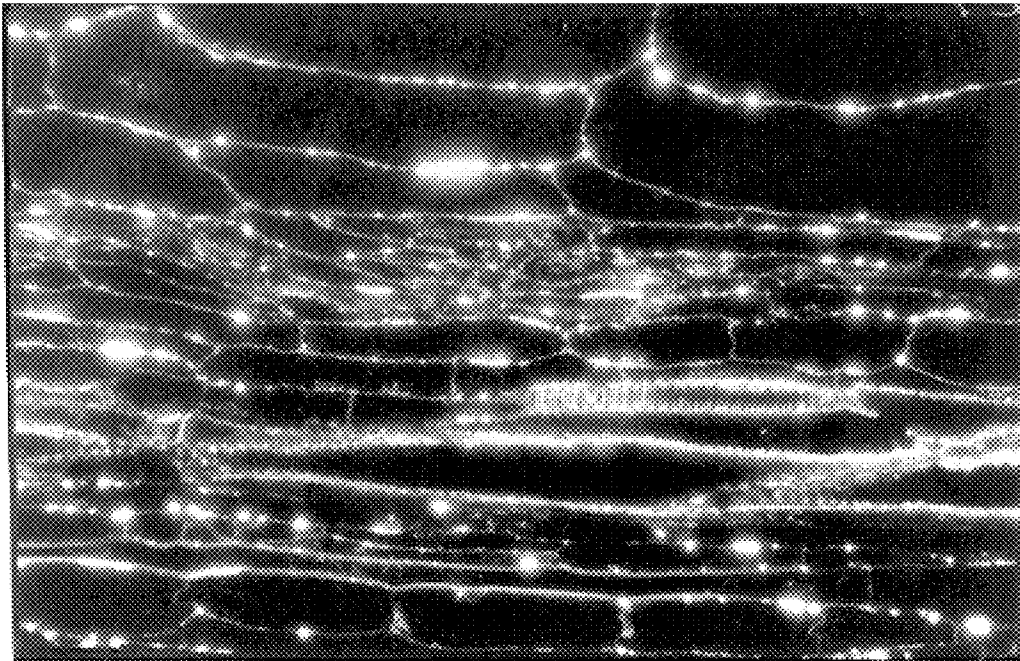
L

Fig. 9d

S7nc



T



L

Fig. 9e

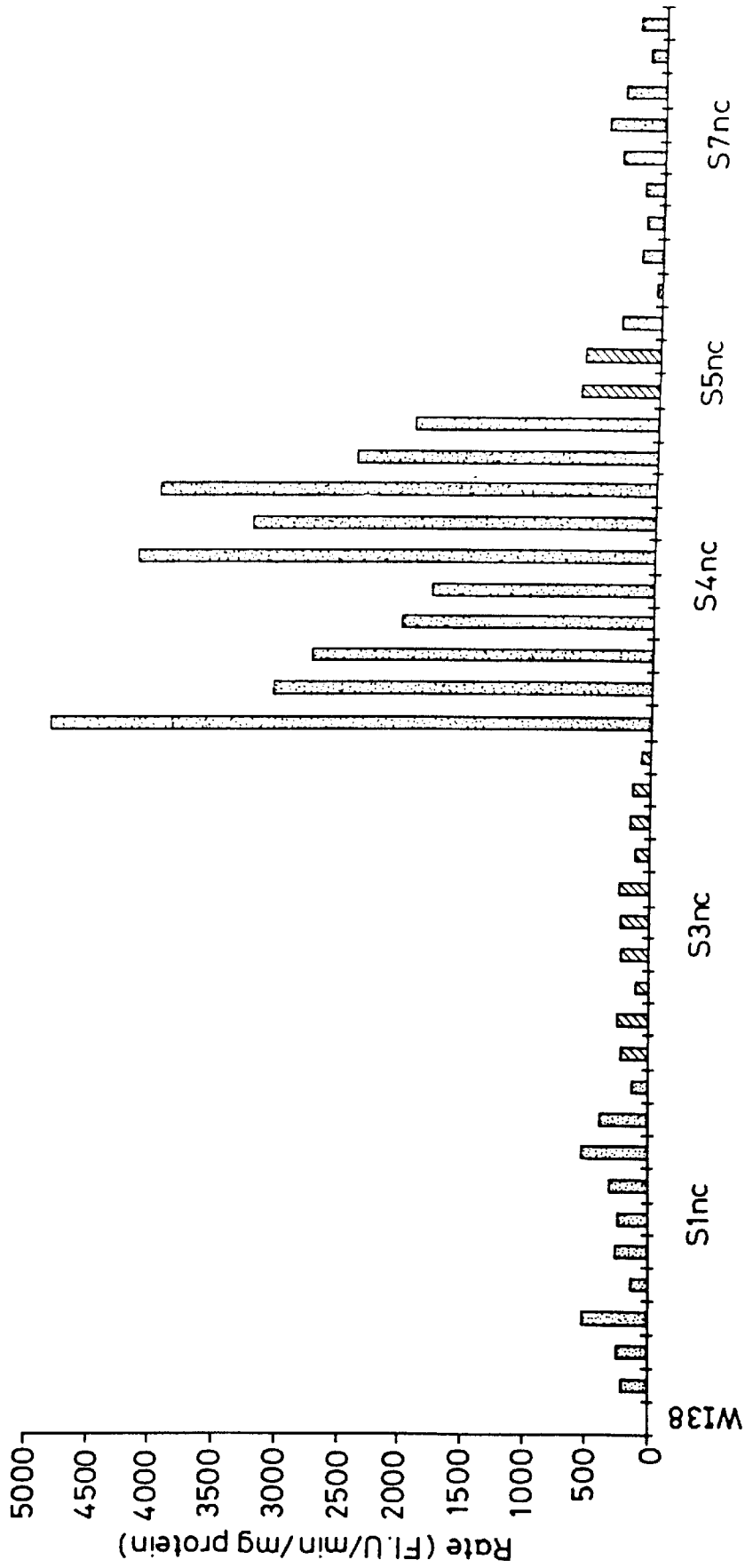


Fig.10

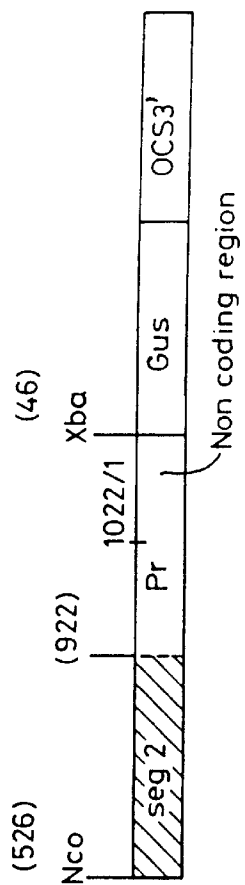


Fig.11

SC3Tr

[EcoRI, NcoI, BamHI, SmaI, SalI]

5' 809

[HindIII, XbaI, XhoI]

3' 947

Fig.12a

SC5Tr

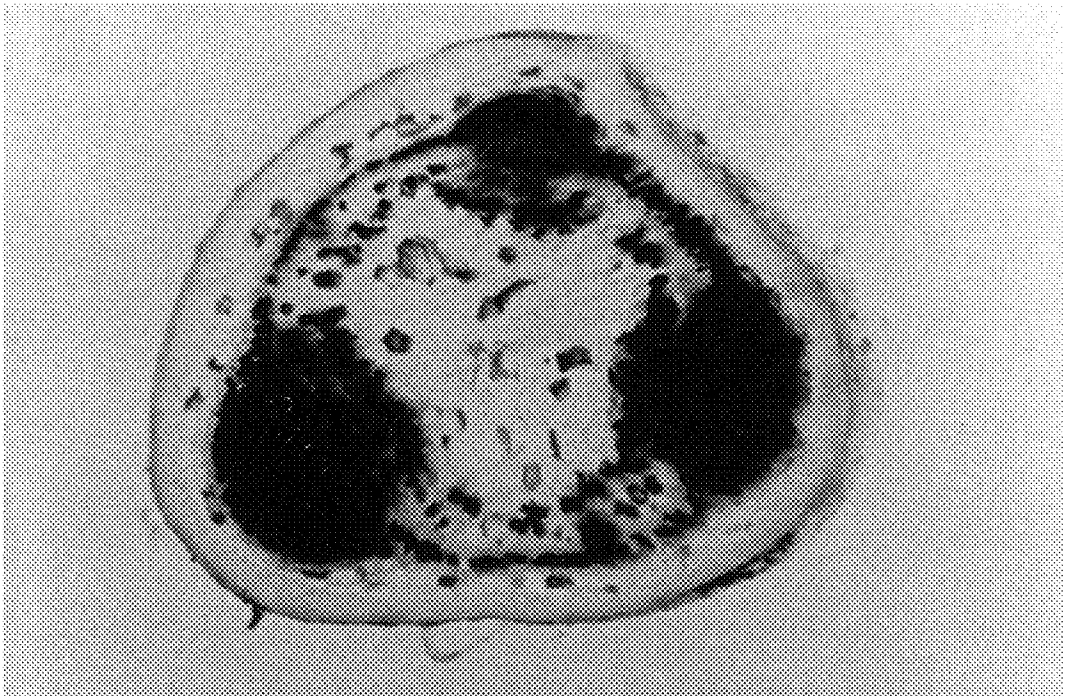
[EcoRV, NcoI, BamHI, SmaI, EcoRI, XbaI]

5' 791

[NotI, HindIII, EcoRV]

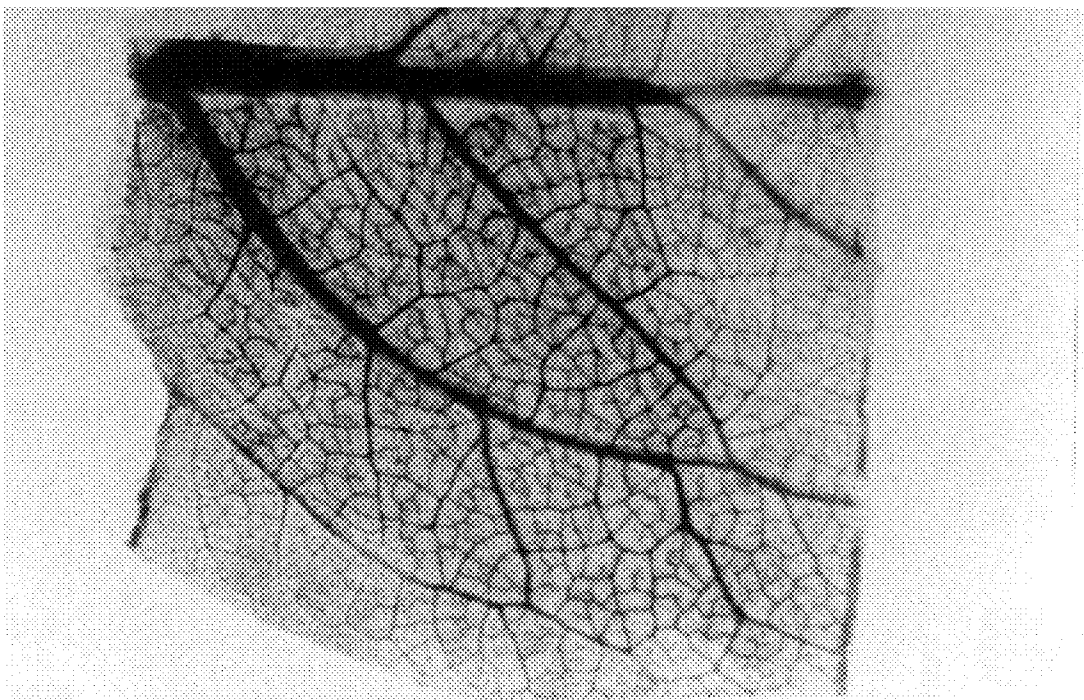
3' 953

Fig.12b



Stem

Fig.13a



Leaf

Fig.13b



Fig.13c

Stolon

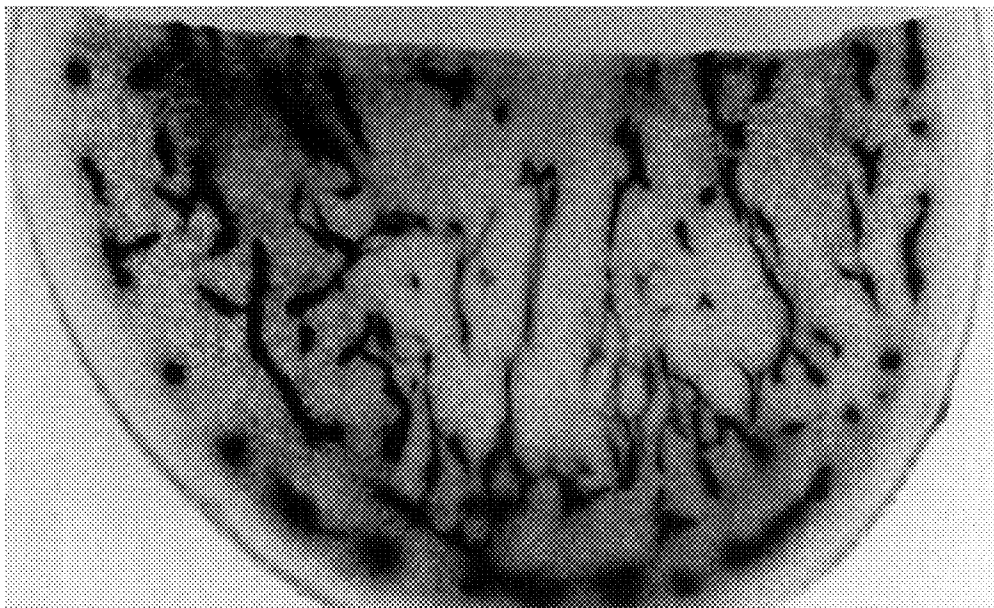


Fig.13d

Tuber

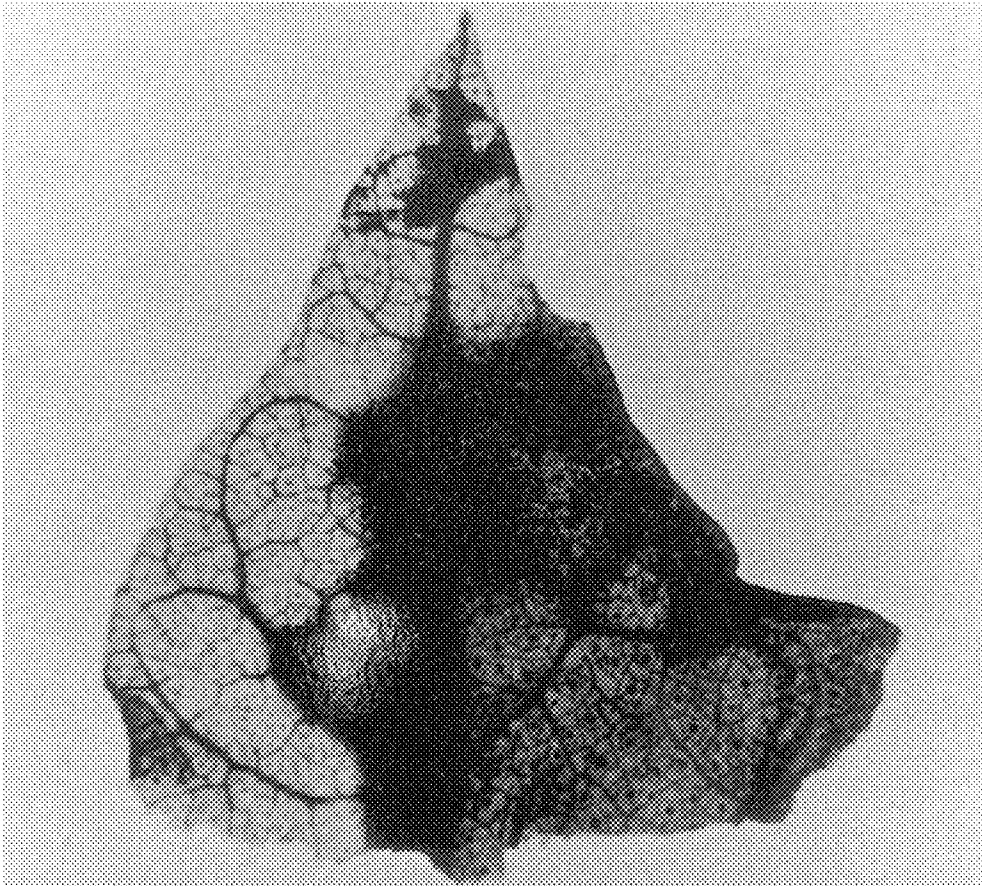


Fig. 14

1	TAAGTTTAGC	GGGGGAAAAA	GGACAGTTGA
61	ATGTTGTCAG	ATGCATGTTG	TAATGCTTGT
121	TGATGATGGA	AACTTAAAGC	TTAATACTAC
181	GGTTCTTTGT	TTATCAGGAA	TGCTCATTGT
241	TATTGCCCTA	AATCTGGTAC	TTTATCCAAA
301	TCAAGAATGA	TAAACTCGTA	CACTCTCTAG
361	AACCGCTTAG	GAAGGAACAT	ATGTGATAAG
421	AGTCGGCCCA	ATTCGAGAGG	ACTAGTCTCC
481	TAAACAAAAC	ACATATAAAA	AACCTAAAAA
541	GTGGGAACAG	TTACAAATCT	GCAGTCTCAC
601	CAAGTTTTTCG	AATGTTCTCC	CACCATTCAC
661	TAGCTGACAC	AACCCGTTTT	GACCCAACAT
721	AATCGACTTG	TCCTCAAGTC	GAAAGGAGGG
781	ATTGGAGGTT	GATGGATGAT	TTCCTTGTGT
841	GCTTTTAATG	CCTCTTGAAC	TGTAGCCACA
901	AATTC		

Fig. 15a

TCTGTTGCTG	TTTGCAATTT	TTTAAAGGGT	60
TCATCAACAC	ATTATATGAC	TTGCAGTTGC	120
TTTTGTTTAT	TCACTTACAA	ATACCGGTTG	180
ATGTAGCTAA	AAGCTGGCCG	TTTATAGTTT	240
AACTAAATTT	GGAAACATCA	AATACTTTTT	300
GGTACTCCTG	AAATTTAAAT	CAAATCCAA	360
AACTGAAATT	TCGATTAAct	ATTACAAGAT	420
GATTACAAGG	AGTAAATATC	TTAATCTTGA	480
TATAGGAACA	TAATACATAA	ACTAAAAGTT	540
TCCCTAAATT	TGTGAGTCAC	CTTTCACCTA	600
TTTCCCTCCA	CCCGGATTCC	CTCCAATTAA	660
TGGGTTCGTA	TCAATACATC	CGGCCCGGAA	720
GAATTATTGT	GCCAAGCAAA	AAGCCATTCG	780
TTGAAAGCTT	CAAAGATCC	GGCCAAATCA	840
ACACCACTTT	GAAACCTCAA	ATCTGTTTTG	900
			905

Fig.15b

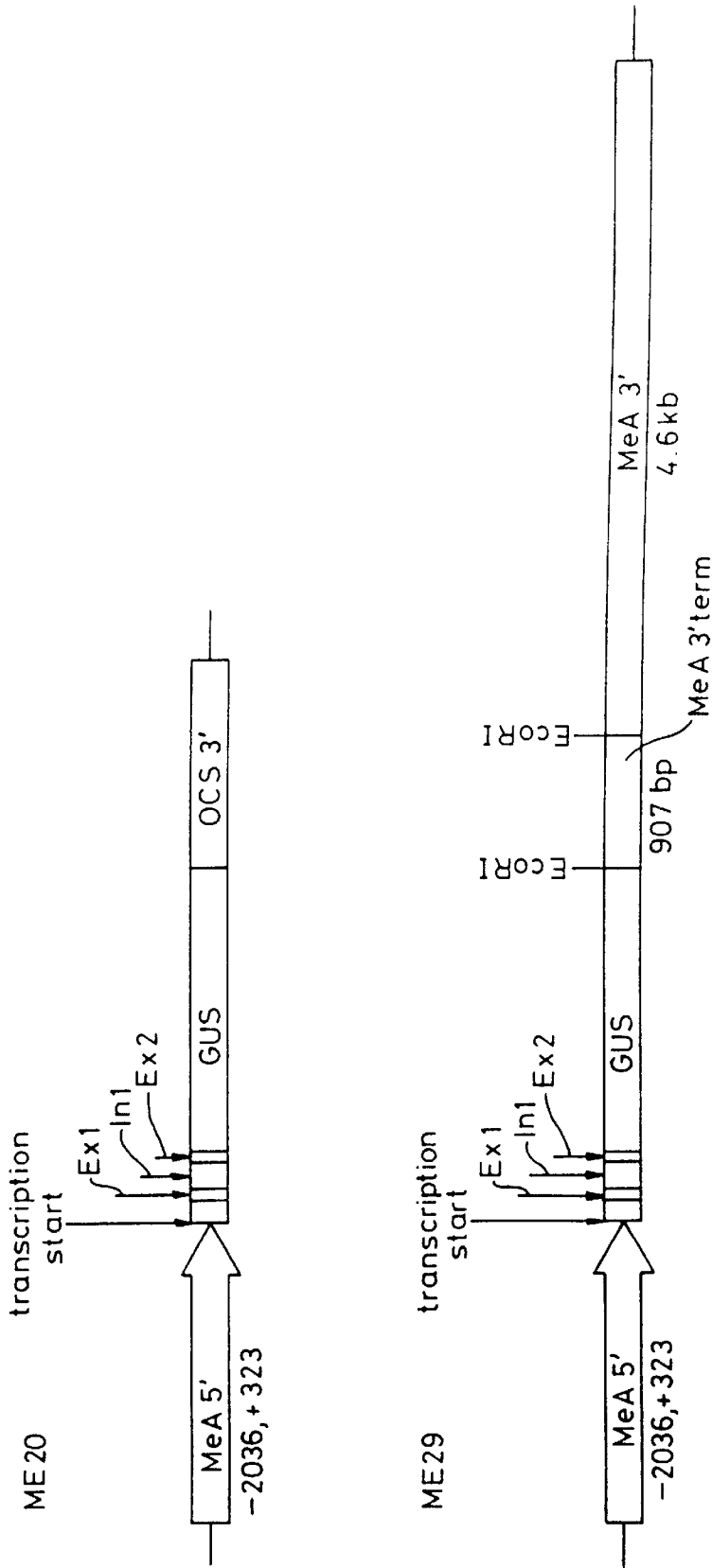


Fig. 16

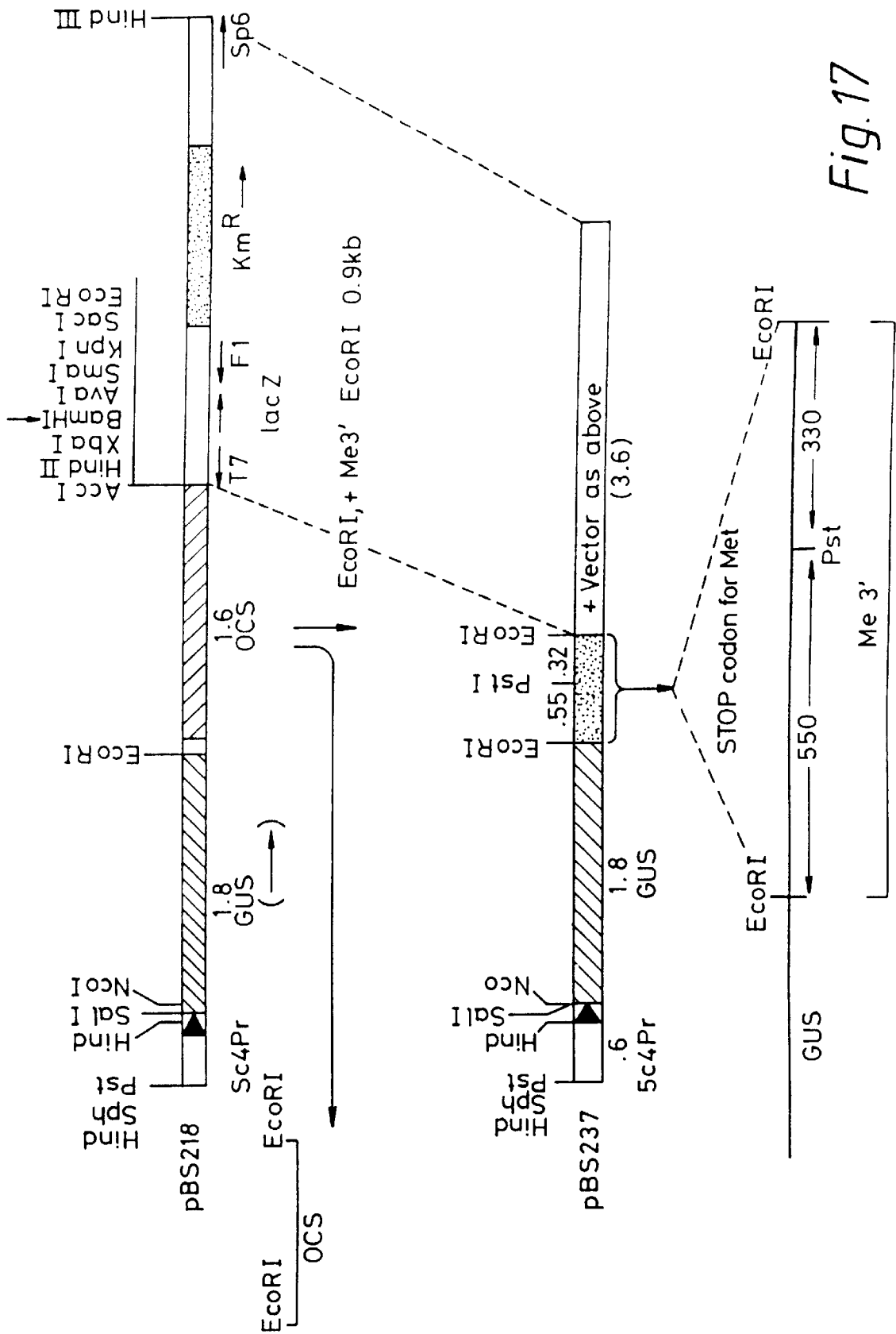


Fig. 17

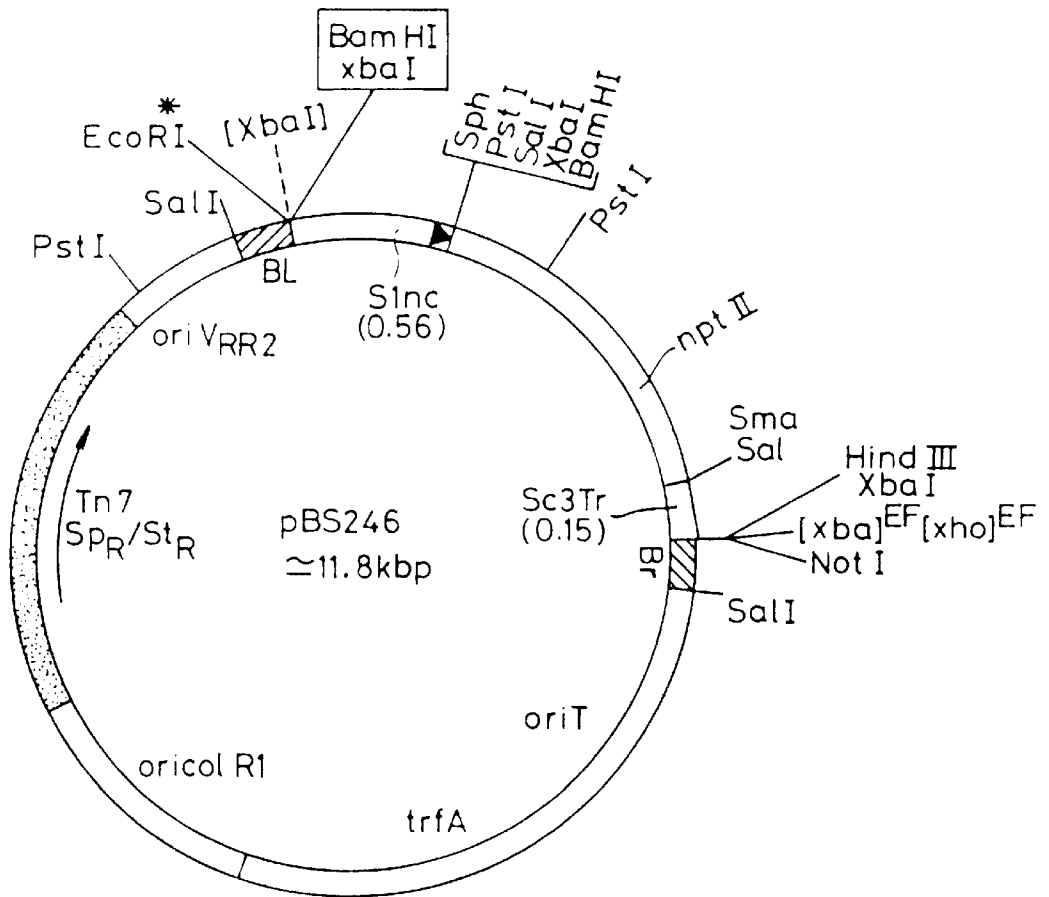
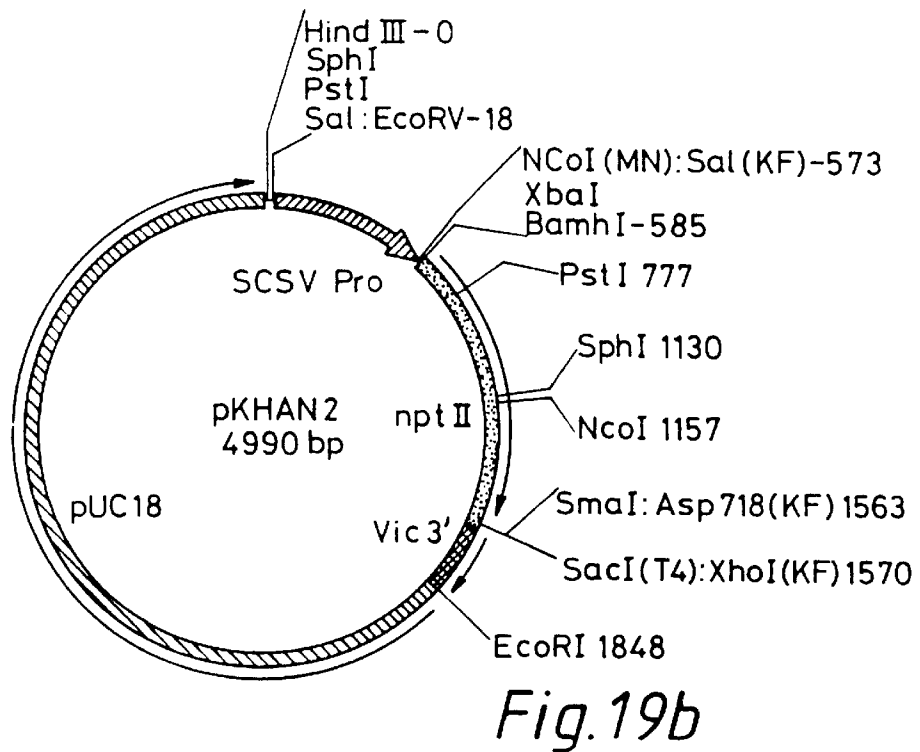
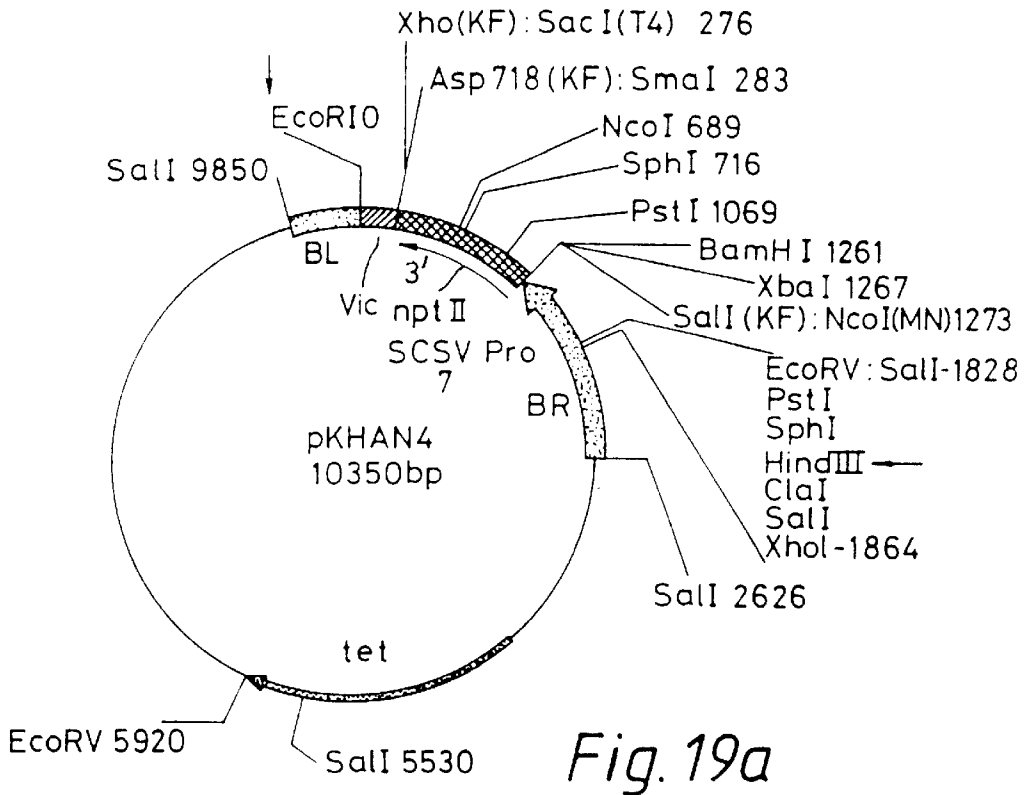


Fig. 18



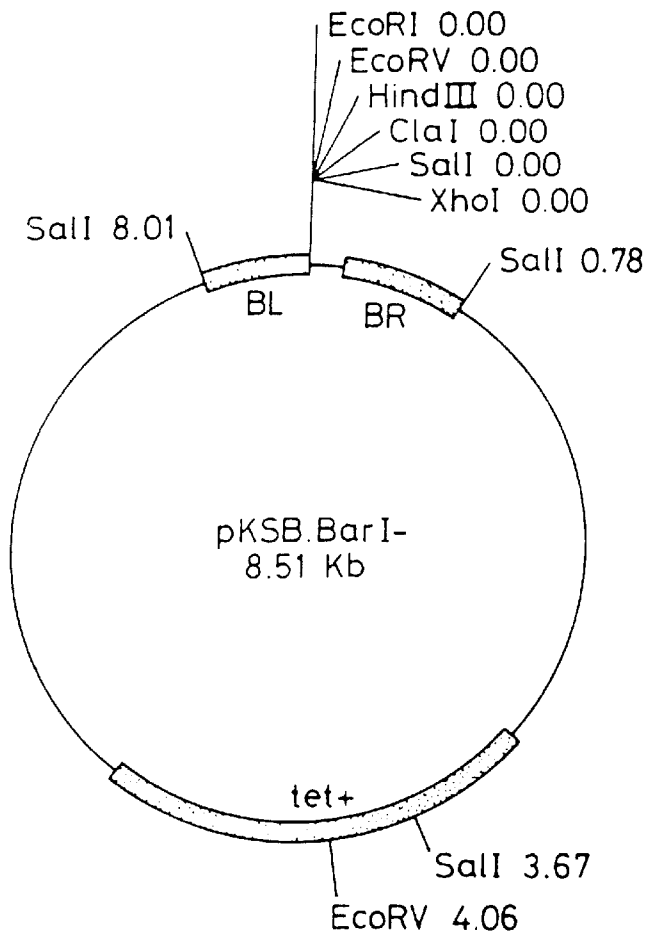


Fig. 19c

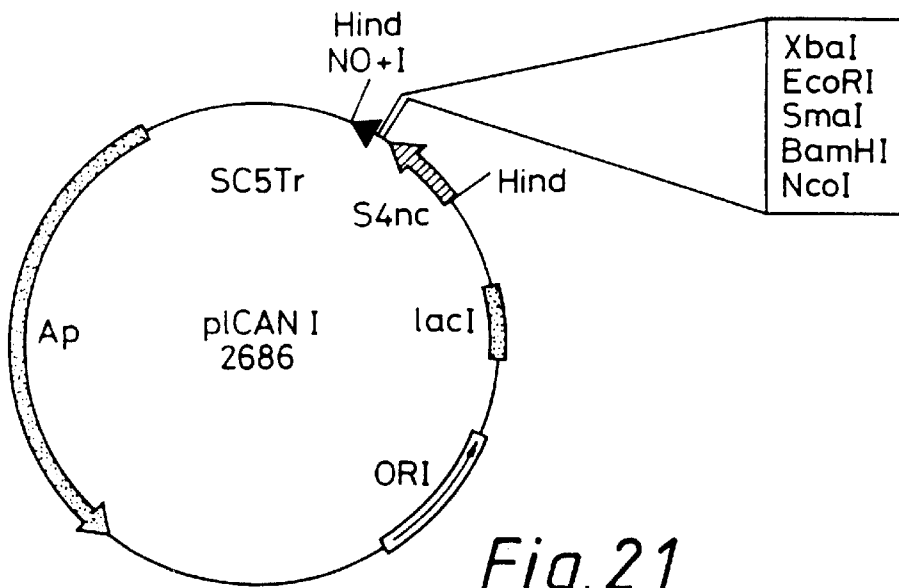


Fig. 21

35S Prm NPTII 35S Trm

SC1 Prm NPTII SC3 Trm

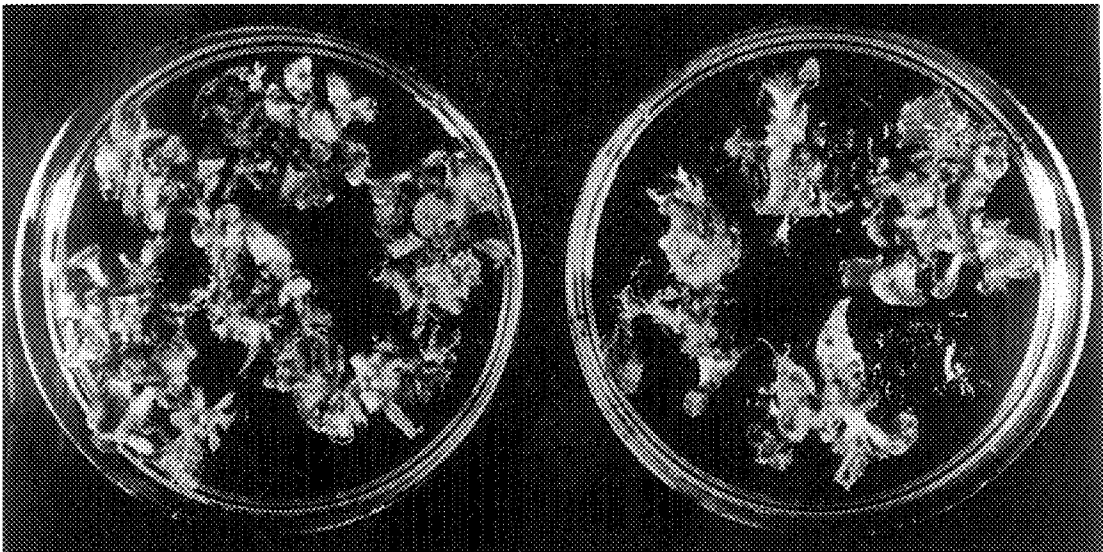


Fig. 20

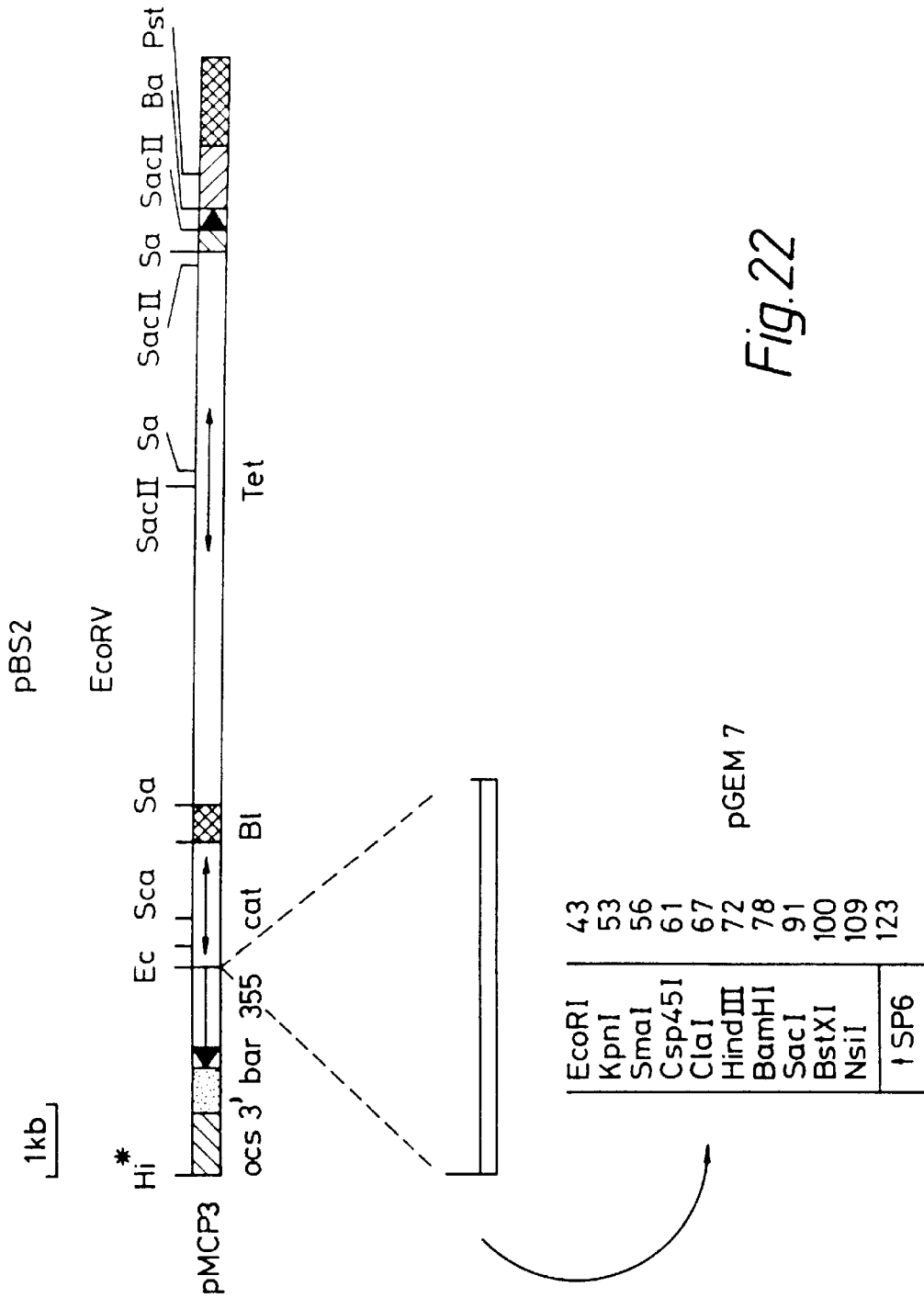


Fig. 22

PLANT TRANSCRIPTION REGULATORS FROM CIRCOVIRUS

The present invention relates generally to a novel range of transcription regulators and transcription regulator-like sequences operable in plants. More particularly, the present invention is directed to transcription regulators and transcription regulator-like sequences of viral origin and, even more particularly, of nanovirus origin. The transcription regulators and transcription regulator-like sequences of the instant invention are useful in genetic engineering of plants and in particular leguminous plants such as to facilitate or control expression of foreign genes. The transcription regulators and transcription regulator-like sequences of the present invention are also useful in facilitating different levels of expression in different plant tissue types.

Bibliographic details of the publications referred to by author in this specification are collected at the end of the description. Sequence Identity Numbers (SEQ ID Nos.) for the nucleotide sequences referred to in the specification are defined following the bibliography.

Throughout this specification, unless the context requires otherwise, the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element or integer or group of elements or integers but not the exclusion of any other element or integer or group of elements or integers.

Transcription regulators are molecules, and generally nucleotide-based molecules, which facilitate and modulate expression of genetic sequences at the level of transcription. Transcription regulators include promoters and termination and polyadenylation sequences amongst other effectors and facilitators of transcription.

Promoters are specific nucleotide sequences to which RNA polymerase binds to initiate RNA synthesis in cells. They contain the start site for RNA synthesis and the genetic signals to initiate polymerase mediated RNA synthesis. In addition, sequence specific DNA-binding proteins are presumed either to inhibit or to stimulate the initiation of RNA synthesis by binding next to the promoter and affecting the binding of the polymerase to the promoter. Terminator sequences refer to termination and polyadenylation sequences and are required for transcription of functional mRNAs. Termination sequences are located downstream (i.e. at the 3' end) of a gene and are recognized by RNA polymerase as a signal to stop synthesizing mRNA. Polyadenylation sequences are signals required for polyadenylation of eukaryotic mRNA molecules following transcription.

A viral promoter widely used to facilitate foreign gene expression in plants is the cauliflower mosaic virus (CaMV) 35S promoter (Odell et al, 1985), which is derived from a double-stranded DNA plant virus. The use of this promoter in plants and plant cells is well documented (Benfey and Chua, 1990; Higgins and Spencer, 1991). However, despite the apparent usefulness of this promoter, it is not functional in all plants and is particularly poorly operable in leguminous plants. There is a need, therefore, to identify other promoters, such as of viral origin, which are operable in plants and particularly leguminous plants. There is also a need to modulate levels of expression of genes and other genetic sequences within plant cells.

BRIEF DESCRIPTION OF THE INVENTION

Accordingly, one aspect of the present invention is directed to a genetic construct comprising a nanovirus promoter or promoter-like sequence and which is operable

in a plant cell wherein said nanovirus comprises a multi-component DNA genome.

In a related aspect of the present invention, there is provided a genetic construct comprising a nanovirus promoter or promoter-like sequence and a termination and/or polyadenylation sequence, which sequences are operable in a plant cell.

A nanovirus is a non-geminated single stranded (ss) DNA plant virus (Table 1), distinct from caulimoviruses which have a double stranded genome, and geminiviruses, the only other known ssDNA plant viruses, which have geminated particles (Chu et al., 1994). As used herein, the nanovirus group is considered to include subterranean clover stunt virus (SCSV) (Chu and Helms, 1988), banana bunchy top virus (BBTV) (Thomas and Dietzgen, 1991; Harding et al. 1991; 1993; Bums et al. 1993) and milk-vetch dwarf virus (MDV) (Isogai et al. 1992; Sano et al. 1993) and faba bean necrotic yellows virus (FBNYV) (Katul et al., 1993).

In a particularly preferred embodiment, the nanovirus contemplated for use in accordance with the present invention comprises more than two DNA components or segments.

The present invention is particularly directed and hereinafter described with reference to subterranean clover stunt virus (hereinafter abbreviated to "SCSV") as a representative of the nanovirus group. This is done, however, with the understanding that reference to SCSV includes reference to all other suitable members of the nanovirus group to which the instant invention extends. Preferred members of the nanovirus group such as SCSV comprise more than two DNA components or segments. Reference hereinafter to "SCSV" also includes and extends to all naturally occurring or artificially induced mutants, derivatives, parts, fragments, homologues or analogues of the virus which still retain at least one suitable promoter and/or termination and/or polyadenylation sequences.

Accordingly, a particularly preferred embodiment of the present invention contemplates a genetic construct comprising an SCSV promoter or promoter-like sequence and which is operable in a plant cell.

A related aspect of the present invention is directed to a genetic construct comprising an SCSV promoter or promoter-like sequence and a termination and/or polyadenylation sequence, which sequences are operable in a plant cell.

The term "genetic construct" is used in its broadest sense to include any recombinant nucleic acid molecule such as an isolated nucleic acid molecule, vector, expression vector or binary vector. It may comprise solely the nanovirus promoter or may contain one or more promoters in association with regulatory and/or reporter sequences.

The genetic construct may be double or single stranded DNA, in linear or covalently closed circular form. As stated above, it may comprise only the promoter or promoter-like sequence or may carry other heterologous or homologous transcription regulator sequences and/or heterologous structural gene sequences including promoters associated with SCSV. By "homologous" is meant a gene sequence naturally associated with the SCSV promoter. "Heterologous" means a "foreign" gene relative to the promoter or a gene not otherwise normally associated with the SCSV promoter. In a preferred embodiment, the foreign gene is also foreign to SCSV. Examples of foreign genes include genes which facilitate resistance to insects or other pest infestation, enhance resistance to insecticides or herbicides, promote frost resistance, alter flower or petal colour, decrease the rate of senescence, especially in cut flowers, increase or enhance

levels of certain proteins and/or ribozymes. More particularly, the foreign genes include:

- a) a resistance gene against plant viruses, bacteria, fungi, nematode and other pathogens;
- b) a plant virus resistance gene including a synthetic gene from and against alfalfa mosaic virus, subterranean clover stunt virus, subterranean clover mottle virus, subterranean clover red leaf virus, potato leafroll virus, tomato spotted wilt virus, bean yellow mosaic virus, white clover mosaic virus, clover yellow vein virus, potato viruses x, y, s, m and a, cucumber mosaic virus, rice ragged stunt virus and barley yellow dwarf virus;
- c) a gene to improve nutritional value of plants such as sunflower high sulphur gene SF8;
- d) a bloat resistance gene;
- e) an antibody gene;
- f) a cereal thionin and ribosome inactivating protein gene;
- g) an insect resistance gene including BT toxin gene and proteinase inhibitor gene from *Nicotiana glauca*;
- h) a selectable marker gene such as those conferring resistance to kanamycin, phosphinothricin, spectinomycin and hygromycin;
- i) a reporter gene such as GUS, CAT and pigment genes;
- j) a gene encoding a regulatory protein which modulates expression of a gene in plant cells.

The present invention further contemplates a genetic construct comprising two heterologous genes operably linked to the same or different nanovirus promoters operable in a plant cell. Preferably the promoter or different promoters are from a nanovirus with a genome comprising more than two components or segments. Most preferably the promoter or different promoters are from SCSV and in particular are selected from segments 1 to 7 of SCSV as defined by SEQ ID NOs. 1 to 7. (See below).

The genetic constructs may also comprise a termination or polyadenylation sequence operably linked to one or both of the heterologous genes. In one embodiment, the termination and/or polyadenylation sequence is the same for each gene. In an alternative embodiment the termination and/or polyadenylation sequence is different for each gene. Most preferably the termination and polyadenylation sequence is selected from segments 1 to 7 of SCSV as defined by SEQ ID NOs. 1 to 7 (See below). In yet another embodiment at least one termination and polyadenylation sequence is from the MeA 3 gene of *Flaveria bidentis* (see below).

The term "transcription regulator" is used in its broadest sense to include promoters, termination and polyadenylation sequences and other effectors and facilitators of transcription of genetic sequences. As with promoters contemplated by the present invention, the termination and polyadenylation sequences may be of SCSV origin and may be naturally associated with a corresponding promoter from SCSV or may be associated with another promoter of SCSV. Alternatively, the termination and/or polyadenylation sequences may be derived from non-SCSV sources. A particularly preferred terminator comprises the 3' nucleotide sequence of the MeA3 gene of *Flaveria bidentis* which codes for an NADP-malic enzyme of C4 photosynthesis (Hatch, 1987). The nucleotide sequence of the terminator region of the MeA gene is shown in FIG. 15. The combination of an SCSV promoter with, for example, the *F. bidentis* MeA gene terminator sequence results in a high level of expression especially in monocotyledonous plants relative to constructs without the terminator sequence.

The foreign gene may also be in the antisense orientation so as to facilitate reduced levels of endogenous plant gene

products. In this regard, "gene" may be ten base pairs in length, tens of base pairs in length, hundreds of base pairs in length or a full length or near full length gene but in a reverse orientation relative to the promoter. The foreign gene may also be placed in the "isense" orientation for co-suppression of a target gene.

According to another aspect of the present invention, there is provided a genetic construct comprising an SCSV promoter or promoter-like sequence operable in a plant cell and at least one restriction endonuclease site downstream of said promoter to facilitate insertion of a heterologous gene such that said gene is operably linked to said promoter. In an alternative embodiment, the genetic construct comprises an SCSV promoter or promoter-like sequence operable in a plant cell and a heterologous gene operably linked to said promoter. In both embodiments, the term "gene" includes those directing the synthesis of oligonucleotides such as those useful in antisense techniques as well as ribozymes.

In still a further embodiment of the present invention, there is contemplated a genetic construct comprising an SCSV promoter or promoter-like sequence operable in a plant cell and at least one restriction endonuclease site downstream of said promoter to facilitate insertion of a heterologous gene such that said gene is operably linked to said promoter and a termination and/or polyadenylation sequence positioned such that same sequence is at the 3' end relative to said heterologous gene to facilitate expression of said heterologous gene. Preferably, the termination sequence is from SCSV. Alternatively, the terminator sequence is from the *F. bidentis* MeA3 gene.

Plants contemplated by the present invention include both monocotyledonous and dicotyledonous species. The present invention also extends to leguminous and non-leguminous plants although leguminous plants are preferred.

The SCSV genome comprises at least seven distinct circular ssDNA components described as segments 1-7. The size of these segments range from about 988 to about 1022 nucleotides. Each of the seven DNA components of SCSV contains one major open reading frame of the viral sense and a non-coding region of various lengths containing a conserved potential stem and loop structure (FIGS. 1 and 2; Table 2). Each transcription unit contains a typical TATA box and a polyadenylation signal for start and end of transcription, respectively (Table 2).

Because the DNAs are circular, the sequences in the non-coding regions comprise the promoters and the terminator signals which vary with different DNA components (Table 2). The TATA boxes and the stem-loops of the two replicase-associated protein genes in segments 2 and 6 are quite different from those of the other genes. In contrast, the stem-loops and TATA boxes are the same in segments 1, 3, 4, 5 and 7. All the DNAs, except those of segments 2 and 6, also share a common sequence (known as the common region) in the non-coding region (FIGS. 1 and 2).

The present invention, therefore, extends to each of the seven promoters and to termination and polyadenylation sequences on segments 1-7 of SCSV. The nucleotide sequences of segments 1-7 are shown in FIG. 6 and are defined in SEQ ID NOs. 1-7, respectively.

Segment 5 was identified as the coat protein gene based on N-terminal amino acid sequence and amino acid composition data (Chu et al., 1993a). Segments 2 and 6 encode proteins containing the characteristic NTP-binding motifs and thus are predicted to be the putative viral replication-associated protein (RAP) genes. The remaining 4 DNA components are unrelated to each other or to segment 2, 5 and 6, based on their distinctive deduced amino acid

sequence. The SCSV DNAs have no significant nucleotide sequence homology with the genomes of geminiviruses although some homology exists at the deduced amino acid level.

The replicative competency of SCSV has been demonstrated (Chu et al., 1993b). Since the SCSV virion DNA is single-stranded and the transcripts are of viral sense, the first likely biosynthetic event after uncoating is likely to be the synthesis of the replicative form DNA using host DNA polymerase. (The DNAs of SCSV have the ability to self prime in dsDNA synthesis [Chu and Helms, 1988]). Host RNA polymerase is thought to bind to the promoters initiating RNA transcription followed by synthesis of the viral proteins required for virus multiplication.

In a particularly preferred embodiment of the present invention, there is contemplated an SCSV promoter or promoter-like sequence comprising a nucleotide sequence selected from within SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6 and SEQ ID NO: 7 and/or genetic constructs comprising same.

A "promoter-like sequence" as used herein includes any functional mutant, derivative, part, fragment, homologue or analogue of a naturally occurring SCSV promoter. Promoter-like sequences contemplated herein include single or multiple nucleotide substitutions, deletions and/or additions to an SCSV promoter, provided that the said promoter-like sequences retain at least 35%, preferably at least 45%, more preferably at least 55%, even more preferably at least 65–70% and still more preferably at least 85–95% or greater promoter activity compared with the corresponding wild-type SCSV promoter.

In yet another embodiment, there is provided a genetic construct comprising an SCSV promoter or promoter-like sequence and which is operable in a plant cell, said promoter or promoter-like sequence corresponding to all or part of any one of SEQ ID NO: 1 to 7 or capable of hybridising under a range of stringency conditions, ranging from high to low stringency conditions to at least one of SEQ ID NO: 1 to 7. Conveniently, a mutant, derivative, part, fragment, homologue or analogue of an SCSV promoter is defined as being functional in a plant cell and capable of hybridising under a range of at least high to low stringency conditions to at least one of SEQ ID NO: 1 to 7.

In a particularly preferred embodiment, the genetic construct further comprises a termination and/or polyadenylation sequence from SCSV or from non-SCSV source and which enhances or other facilitates expression of a gene operably linked to said promoter.

For the purposes of defining the level of stringency, reference can conveniently be made to Sambrook et al (1989) which is herein incorporated by reference where the washing steps at pages 9.52–9.57 are considered high stringency. A low stringency is defined herein as being in 0.1–0.5% w/v SDS at 37–45° C. for 2–3 hours. Depending on the source and concentration of nucleic acid involved in the hybridisation, alternative conditions of stringency may be employed such as medium stringent conditions which are considered herein to be 0.25–0.5% w/v SDS at $\geq 45^\circ$ C. for 2–3 hours or high stringent conditions as disclosed by Sambrook et al (1989).

Another embodiment of the present invention contemplates a method of expressing a foreign gene in a plant cell, said method comprising introducing into said plant cell a genetic construct comprising and SCSV promoter or promoter-like sequence operable in said plant cell and operably linked to said foreign gene. In a further

embodiment, multiple SCSV promoters are used to drive one or more transgenes without antagonism. In yet a further embodiment, the SCSV promoter is associated with the SCSV segment 2 gene in order to enhance the expression of the foreign gene. In another embodiment, the genetic constructs further comprises one or more termination and/or polyadenylation sequences which are located at the 3' end of the foreign gene. These sequences enhance or otherwise facilitate expression of the foreign gene. The termination and/or polyadenylation segment may be from SCSV or from another source such as the *F. bidentis* MeA gene.

In still yet another embodiment, the present invention contemplates a transgenic plant carrying an SCSV promoter or promoter-like sequence as hereinbefore defined in its genome and optionally a termination and/or polyadenylation sequence to enhance expression of a gene downstream of said promoter. Preferably, the transgenic plant exhibits altered characteristics due to expression of a genetic sequence such as a gene, oligonucleotide, or ribozyme downstream of the SCSV promoter.

DETAILED DESCRIPTION OF THE INVENTION

The present invention is further described by reference to the following non-limiting figures and/or examples. Reference herein to a promoter region from SCSV is abbreviated to "S" for SCSV, the genome segment number (e.g. 1, 3, 4, 5 and 7) and "nc" for non-coding region. For example, the promoter from SCSV genome segment 1 is defined as "S1nc". Terminator sequences for particular SCSV genome segments are indicated for example, as follows: "SC1Tr" or "SC5Tr" for the terminator sequences for segments 1 and 5, respectively. Genetic constructs comprising an SCSV promoter, a reporter gene such as GUS and a terminator sequence such as from SCSV is abbreviated to "SCSV:GUS:SCTr" or "SCSV:GUS:SCSVTr". Specific promoters and termination sequences are defined as above, for example S4nc:GUS:SC1Tr or S4nc:GUS:Me3", "S4nc:GUS:Me3". In the latter construct the terminator sequence from the MeA gene of *Flaveria bidentis* is used, referred to herein as "Me3".

In the Figures:

FIG. 1 is a schematic representation showing the structures and transcription units found in a representative DNA component of a typical geminivirus and SCSV, both of which contain a ssDNA genome.

FIG. 2 is a schematic representation showing the seven DNA segments found in the genome of SCSV in a linear form, indicating the positions of the stem-loop structure, the common region, the open reading frame (ORF), the TATA box and the termination and polyadenylation signals on each DNA.

FIG. 3 is a schematic representation showing the construction of the seven SCSV DNA non-coding region: β -glucuronidase (GUS) fusion expression vectors for transformation into tobacco plants. The amplified PCR fragments were separately cloned in front of the GUS gene in pHW9 at the BamHI (B) and NcoI (N) sites as indicated. The resultant recombinant pHW9 vectors were cut at the EcoRI site and cloned into the EcoRI site of the recipient PGA470 binary vector.

FIG. 4 is a schematic representation showing the construction of the segments 5 and 7 promoter:GUS fusion expression vectors and their deletion derivatives for protoplast studies. DNAs corresponding to the full-length non-coding regions were obtained by PCR and cloned into

pKGO in front of GUS by blunt end ligation at the Sal/I site as indicated. The deletion derivatives were obtained by digesting the pKGO clones containing the full-length sequence with HindIII or PstI on the vector and the appropriate restriction enzymes on the SCSV sequence as indicated. The deleted pKGO constructs were religated after end-filling as required.

FIG. 5 is a schematic representation showing the construction of the recombinant binary pTAB10 vector (pBS150) containing the seg 7 promoter(57nc):GUS fusion gene for transformation into subterranean clover plants. The 57nc:GUS expression cassette was excised.

FIG. 5 is a schematic representation showing the construction of the recombinant binary pTAB10 vector (pBS150) containing the seg 7 promoter(57nc):GUS fusion gene for transformation into subterranean clover plants. The 57nc:GUS expression cassette was excised from the pKGO construct (FIG. 4) by digestion with HindIII and BamHI and blunt-end ligated to pTAB10 at the EcoRI site after end-filling the DNAs.

FIGS. 6(i)–6(xiv) show the complete nucleotide sequences of the seven SCSV DNA circles (SEQ ID NOS:1 to 7). The arrows underlying the sequence indicate the positions at which amplification primers (Table 8) anneal to the circular SCSV DNA, including the direction of amplification, thereby amplifying a single fragment containing a promoter and terminator/polyadenylation signal for the construction of expression cassettes.

FIG. 7 is a copy of a photographic representation showing GUS expression detected by histochemical staining on leaves of transgenic tobacco and subterranean clover transformed with the SCSV seg 7 promoter(57nc):GUS fusion expression cassette.

FIGS. 8A to 8F are photographic representations of histochemical staining for GUS activity in transgenic plants—bright field. Bright field exposures of stained leaf pieces (L), stem sections (S), roots (R) and pollen (P) from tobacco plants transformed with the GUS fusion constructs containing the SCSV promoter regions from segments 1, 3, 4, 5 and 7 referred to as S1nc, S3nc, S4nc, S5nc and S7nc promoter regions and from non-transformed plants (NT). Blue colouration indicates GUS expression. Each leaf, stem or root piece represents an independent transformant (except the top two root pieces of S5nc which could not be separated easily) and the pollen samples were mixtures from two or more transformants. FIG. 8a shows differential expression of GUS in plants transformed with either S4nc or S5nc regions compared to a non-transformed plant (NT).

FIGS. 9A to 9E are photographic representations showing histochemical staining for GUS activity in transgenic plants—dark field. Transverse (T) and longitudinal(L) thin sections of stained, embedded stem pieces from tobacco plants transformed with the GUS fusion constructs containing the component 1 (S1nc), 3 (S3nc), 4 (S4nc), 5 (S5nc), and 7 (S7nc) promoter regions, viewed with a dark field. Pink crystals indicate GUS expression. The stem pieces used.

FIG. 10 is a graphical representation of a fluorometric assay for GUS expression. Fluorometric assay results from leaf extracts of tobacco plants transformed with the GUS fusion constructs containing the component 1 (S1nc), 3 (S3nc), 4, (S4nc), 5 (S5nc), and 7 (S7nc) promoter regions. Each column represents an independent transformant. GUS activities were measured with a Labsystems Fluoroskan at 5 or 10 minute intervals over 60 minutes (or 30 minutes for S4nc) using 4-methylumbelliferyl β -D-glucuronide (MUG)

as the substrate. The rates of GUS activity are expressed as fluorometric units (F.L.U.) per minute per mg of protein. 1000 F.L.U is approximately equal to 825 pmoles of 4-methylumbelliferone (MU).

FIG. 11 is a schematic representation showing the SCSV segment 2 promoter (S2nc) construct. A fragment of segment 2 DNA from NcoI-XbaI was fused to the promoterless GUS vector, pKGO. Pr, promoter; seg 2, segment 2 of SCSV.

FIGS. 12a and 12b are schematic representations showing constructs of SCSV:GUS:SCSV Tr expression vectors. The termination/polyadenylation sequences for segment 3 of SCSV (SC3Tr) and segment 5 (SC5Tr) were amplified by PCR and cut with the respective restriction enzymes and then cloned into recombinant pKGO vector as indicated. The SC3Tr construct was cloned as an EcoRI-XhoI fragment into the pKGO vector containing S1nc:GUS:OCS3' to make S1nc:GUS:SC3Tr. The SC5Tr construct was made as an EcoRV fragment into Vector pKGO containing S4nc:Gus:OCS3' to make S4nc:GUS:S5Tr.

FIGS. 13A to 13D are photographic representations showing GUS expression in potato plant tissues directed by the SCSV segment 4 promoter (S4nc). A. stem; B, leaf, C. stolon; and D. tuber.

FIG. 14 is a photographic representation of GUS expression in cotton leaf directed by the SCSV segment 7 promoter (S7nc).

FIGS. 15(a)–15(b) show the nucleotide sequence of the MeA3's terminator sequence of the *Flaveria bidentis* MeA gene (Me3) set forth in SEQ ID NO: 8. The stop codon is located at the beginning of the sequence. This sequence was engineered in the Chimeric construct to include an EcoRI site: GAATTCGTTTAG. . . . The chimeric constructs thus contained a sequence beginning AATTCGTTTAG.

FIG. 16 is a diagrammatic representation of GUS expression vectors (ME20 and ME29) containing the indicated *Flaveria bidentis* MeA gene regulatory elements.

FIG. 17 is a diagrammatic representation of the construction of S4nc plasmid pBS237 containing the expression cassette S4nc:GUS:Me3'. Plasmid pBS218 was digested with EcoRI to remove OCS3' region and ligated with an EcoRI.

FIG. 18 is a diagrammatic representation of the construction of plasmid pBS246 containing the S1nc:nptII:SC3Tr expression cassette. The SaII-SaII fragment is approximately 8.5–9 kbp; B_L is about 0.5 kbp; B_R is about 0.6 kbp. SC1nc:nptII:SC3Tr is about 1.7 kbp.

FIG. 19a–c are diagrammatic representations of the construction of plasmid pKHAN4 from pKHAN2 and pKSB.bar1. pKHAN4: A HindIII-EcoRI segment containing S7nc (572 bp), nptII coding region (978 bp) and vicillin 3' end (276bp) from pKHAN2 was inserted into binary plasmid pKSB.bar1 to yield pKHAN4; pKHAN2. The nptII coding region (978bp, BamHI-SmaI fragment) from p35SKN was cloned into Asp718 site (blunted with klenow fragment) of pKHAN1 to create pKHAN 2. SCSV Pro=S7nc; pKSB. Bar 1: pTAB10.MCSori1B digested with EcoRI as ligated together.

FIG. 20 is a photographic representation of a selection of Kananmycin resistant tobacco plants on regeneration medium transformed with binary vectors containing either 35S promoter:NPTII:35S terminator sequence (35SPrm:NPTII:35STrm) or S1nc:NPTII:SC3Tr expression cassette. (In the Figures, the abbreviations are 35S Prm NPTII35STrm and SC1 Prm NPTII Sc3 Trm, respectively.

FIG. 21 is a diagrammatic representation of a cloning vector utilising SCSV DNA transcription regulatory signals.

FIG. 22 is a diagrammatic representation of SCSV segment 2 dimer construct pBS2. This construct was created by cloning a tandem repeat of the SCSV segment 2 DNA (containing a whole functional seg 2 transcription unit) into the polylinker site of pGEM7 which was then cloned into a reduced version of the pMCP3 binary vector (Khan et al., 1994).

A summary of the transcription activities facilitated by the SCSV transcription regulatory elements is shown in Table 19.

EXAMPLE 1

SCSV DNA Sequence Determination

The F isolate of SCSV (Chu et al. 1993a) was used for sequence determination. Full-length clones of the SCSV genome components were created from the replicative form (RF) DNA as described by Chu et al. (1993a). Other clones were created from the RF by PCR with SCSV specific primers designed from known sequences.

The dideoxy chain termination method (Sanger et al., 1977) was used to sequence either M13 ssDNA templates (Sambrook et al., 1989) or dsDNA templates prepared by the CTAB method (Del Sal et al., 1989) from clones described above. Sequence analysis was carried out using the University of Wisconsin Genetics Computer Group Sequence Analysis Software Package (Devereaux et al., 1984).

EXAMPLE 2

Plasmid Construction

DNA manipulation techniques used were as described by Sambrook et al. (1989). The entire non-coding regions of all 7 DNA segments of SCSV were amplified by PCR using specific primers (See Table 8) with appropriate restriction enzyme recognition sites for cloning into the plasmid vectors. The amplified DNA fragments were separately cloned into the respective expression vectors upstream of a promoterless GUS reporter gene in the appropriate orientation to produce the SCSV promoter-GUS fusion constructs as shown in the FIGS. 3 and 4. The expression vector pHW9 (FIG. 3) followed by cloning into the binazy vector pGA470 (An et al., 1985) were used for tobacco transformation. The expression vector pKGO was used for GUS expression in protoplasts (FIG. 4) and the binary vector pTAB10 was used for subterranean clover transformation (FIG. 5). pKGO was constructed by cloning the XhoI fragment of pKIWI101 (Janssen and Gardner, 1989) containing the GUS gene and the OCS terminator sequence into the Sal/I site of pJKKm (Kirschman and Cramer, 1988). Corresponding plasmids containing the 35S promoter fused to GUS were used as controls. The junctions of the clones were checked by sequencing. A promoterless GUS construct was used as a control.

Deletion derivatives of the SCSV segments 5 and 7 promoters were made by digesting the full-length non-coding sequence with an appropriate enzyme to produce the desired deletion (FIG. 4).

To investigate the phenomenon of transactivation, the S5nc:GUS expression cassette was excised from recombinant pKGO constructs and cloned into a pGEM plasmid containing the seg 2 RAP coding region expressed from the 35S promoter. The resultant plasmid carrying both the SCSV promoter:GUS and the 35S promoter:seg 2 RAP expression cassettes were electroporated into protoplasts.

EXAMPLE 3

Protoplast Isolation and Transient Gene Expression

Recombinant plasmids were extracted from *E. coli* by alkaline lysis followed by purification through Qiagen columns as described in the Qiagen Plasmid Handbook.

Suspension cell cultures were used to isolate *Nicotiana-plumbaginifolia* (Last et al. 1991) and subterranean clover cv. Woogenellup protoplasts (Chu et al. 1993b). Purified plasmids were electroporated into protoplasts of subterranean clover or *Nicotiana-plumbaginifolia* as described by Taylor and Larkin (1988). Protoplasts were harvested 3 days later and assayed fluorometrically for transient GUS activity using 4-methyl umbelliferyl β -glucuronide as substrate (see below). All experiments were done using duplicate samples per treatment.

EXAMPLE 4

Transformation of Tobacco with SCSV-promoter-GUS Fusion Constructs

The recombinant pGA470 binary constructs containing the various SCSV promoter:GUS expression cassettes were separately transformed into *Agrobacterium tumefaciens* strain LBA4404 (Hoekema et al. 1983) by electroporation as described by Nagel et al. (1990). *Nicotiana tabacum* cv. Wisconsin 38 were transformed and regenerated as described by Ellis et al. (1987).

EXAMPLE 5

Transformation of Subterranean Clover with SCSV-promoter-GUS Fusion construct

The recombinant pTAB10 binary vector containing the S7nc:GUS fusion construct (pBS150) was transformed into *Agrobacterium tumefaciens* strain AGL1 (Lazo et al. 1991) by triparental mating (Ditta et al. 1980). Subterranean clover cv. Larisa was transformed by *Agrobacterium*-mediated transformation and regenerated as described by Khan et al. (1994).

EXAMPLE 6

GUS Assays

Protoplasts were lysed by sonication in the presence of 0.3% v/v Triton X-100 immediately after harvest. GUS activity of the soluble extract was determined in a fluorometric assay using the substrate 4-methyl umbelliferyl β -D-glucuronide (MUG) (Jefferson et al., 1987). Fluorescence was measured using a Labsystem Fluoroskan II spectrophotometer.

GUS expression in intact transgenic tissues was detected by histochemical staining in 5-bromo-4-chloro-3-indolyl- β -glucuronic acid (X-gluc) (Jefferson et al., 1987) and by fluorometric assay of the soluble extract using MUG.

EXAMPLE 7

Sequence of SCSV non-coding Region

The complete sequences of all the 7 known SCSV DNA circles have been determined (FIG. 6). Each DNA contains a non-coding region with signals (TATA boxes) for promoter activity (Table 2). These sequences have not been described or isolated before. Sequence comparison of the non-coding regions comprising these promoters showed that segments 3 and 5 are most similar, sharing 258 conserved nucleotides out of an average of 491 nucleotides in the non-coding regions of the DNAs. Segments 3, 4, 5 and 7 contain 170 conserved bases between them while only 152 bases are conserved between Segments 1, 3, 4, 5 and 7. The sequence variations in the non-coding regions of the SCSV DNAs suggest that the transcription and replication of the different SCSV genes may be regulated differently.

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EXAMPLE 8

Transient Activity of SCSV Promoters in Protoplasts

The promoter activities of two SCSV DNA non-coding regions have been demonstrated directly by transient expression of GUS using SCSV promoter:GUS fusion constructs in subterranean clover (Table 3) and tobacco protoplasts (Table 4). These results showed that both segment 5 and segment 7 promoters are functional in the absence of other SCSV DNA components. The SCSV promoters are also functional in protoplasts of either a natural host (subterranean clover) or a non host (tobacco). In tobacco protoplasts, the segment 7 promoter was similar in activity to the 35S promoter while the segment 5 (coat protein) promoter consistently showed activity about half that of the CaMV 35S promoter (Table 4). However, the activity of both promoters were higher in subterranean clover protoplasts, with the activity of the segment 7 promoter showing up to several times that of the 35S promoter (Table 3), suggesting that SCSV promoters work better in certain legumes than the widely used 35S promoter. The activity of the segment 7 promoter also appeared to be more variable in subterranean clover protoplasts than the others tested.

Plasmids containing various deletion derivatives of the non-coding sequence of segments 5 and 7 fused to GUS were also constructed (FIG. 4) and electroporated into protoplasts (Table 5). GUS assays of protoplasts transfected with these constructs showed that neither the stem-loop nor the common region were necessary for promoter activity although the latter was required for full activity (Table 5). The DNA sequence required for high level promoter activity appears to be less than 300 bp which is smaller than that required for other promoters, such as 35S promoter (Odell et al., 1985).

EXAMPLE 9

Transactivation of SCSV Promoter Activity by SCSV Segment 2 Gene Product

When co-electroporated with a 35S promoter:seg 2 RAP gene construct, the activities of GUS driven by the seg 5 promoter apparently increased by about 2 fold in both subterranean clover and tobacco protoplasts (Table 6). The segment 7 promoter activity may also be increased when co-electroporated with the 35S:seg 2 RAP construct but further experiments are needed to confirm this.

Transactivation of GUS activity was also apparently observed when the S5nc:GUS construct was co-electroporated with a binary vector plasmid (pBS2) containing a tandem repeat (dimer) of the segment 2 DNA (Table 6). A map of SCSV segment 2 dimer construct -pBS2 is shown in FIG. 22. This construct was created by cloning a tandem repeat of the SCSV segment 2 DNA (containing a whole functional seg 2 transcription unit) into the polylinker site of pGEM7 which was then cloned into a reduced version of the pMCP3 binary vector (Khan et al., 1994). The results

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suggest that both SCSV promoters are expressed concurrently. Thus, different SCSV promoters can either be used in combination with a 35S promoter or be used simultaneously to facilitate concurrent expression of multiple transgenes in plants. In contrast, reduced transgene activity has been observed when the 35S promoter is used in multiple or multiple copy transgenes (Linn et al., 1990; Matzke and Matzke, 1991; Scheid et al., 1991; Carvalho et al., 1992).

EXAMPLE 10

Activity of SCSV Promoters in Transgenic Plants

All the SCSV promoters, except those from segments 2 and 6, have been shown to be capable of driving expression of transgenes in tobacco plants (FIG. 7). The level of activity of the promoters measured by the MUG assay varied from plant to plant and from one promoter to another but is generally lower than that of the 35S promoter (Table 7).

Histochemical staining of intact transgenic tobacco tissues showed that the activity of the S4nc promoter appears to be constitutive and GUS activity was detected in all plant organs. The others are generally restricted to the vascular tissues although expression is also detected in pollen.

In transgenic subterranean clover plants expressing the S7nc:GUS gene construct, histochemical staining showed that GUS activity is found in leaves, stems and petioles. The distribution of GUS activity is mostly constitutive although in some tissues, the activity is largely in vascular tissues (FIG. 7). In these plants, the level of promoter activity also varies from plant to plant but the activity is generally comparable to that of the 35S promoter.

These results indicate that the SCSV promoters provide a choice of promoters that can be used either independently or simultaneously to control the expression of one or more foreign genes in a wide range of plants and tissue types. Legumes are a major target for application. The activity of these promoters also can be enhanced by the presence of the seg 2 gene product. Thus, these promoters appear to have significant advantages over the CaMV 35S promoter, both in levels of expression, size and in overcoming some negative features of the 35S promoter. They would be applicable in a wide range of transgenic applications.

TABLE 1

Properties of plant viruses with small and multiple encapsidated circular ssDNAs (Plant Nanoviruses)					
Virus	Hosts	Vector	No. of circles	Size (kb)	Coat protein (kDa)
FBNYV	Legumes	Aphids	2+	1	22
MDV	Legumes	Aphids	1+	1	21
SCSV	Legumes	Aphids	7	1	19
BBTV	Monocots	Aphids	6+	1-1.2	20
CFDV	Monocots	Planthopper	1+	1.3	25

Compiled from data presented at the Sixth International Congress of Plant Pathology, Montreal, July, 1993. FBNYV=faba bean necrotic yellow virus, MDV=milk vetch dwarf virus, SCSV=subterranean clover stunt virus, BBTV=banana bunchy top virus, CFDV=coconut foliar decay virus.

TABLE 2

Transcription units and putative gene functions of the SCSV DNA segments

DNA Segment	Size (bases)	Segment Function	Non-Coding Region (bases)	TATA Box		ORF		Termination	Polyadenylation	
				Pos ^a	Sequence	Pos ^b	# aa	Mr (kDa)	Codon	Signal
1	1001	Unknown	661	201	TATAAAAT ^c	48	112	12.7	TGA ^f	AATTAT ^h
2	1022	Replication	178	-8	TATATAT ^d	102	280	32.5	TGA ^f	AATAAAA ⁱ
3	991	Unknown	495	326	TATAAAAT ^c	57	164	19.1	TGA ^f	AATAAAA ⁱ
4	1002	Unknown	539	285	TATAAAAT ^c	71	153	17.7	TAA ^g	AATAAAA ⁱ
5	998	Coat protein	487	330	TATAAAAT ^c	48	169	18.7	TAA ^g	AATAAAA ⁱ
6	1017	Replication	158	-7	AATATAA ^e	66	285	33.5	TGA ^f	AATAAAA ⁱ
7	988	Unknown	546	324	TATAAAAT ^c	67	146	16.9	TAA ^f	AATAAAA ⁱ

^aPosition of the TATA box is the number of bases from the first nucleotide of the stem-loop to and including the first base of the TATA box. See FIG. 1 for a graphic presentation of the genome segments;

^bPosition of the ORF is the number of bases from the first base of the TATA box to and including the first base of the initiation codon;

^cSEQ ID NO: 9;

^dSEQ ID NO: 10;

^eSEQ ID NO: 11;

^fSEQ ID NO: 12;

^gSEQ ID NO: 13;

^hSEQ ID NO: 14;

ⁱSEQ ID NO: 15.

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TABLE 3

SCSV promoter directed GUS activity in subterranean clover protoplasts

Treatments	GUS Activities				
	Expt 1		Expt 2		Average
	Act	% 35S	Act	% 35S	% 35S
No DNA	10	0%	13.1	0%	0%
35S:GUS	27.3	100%	36.6	100%	100%
S5nc:GUS	22.6	73%	40.2	116%	95%
S7nc:GUS	36	147%	117	385%	266%

All experiments were done using duplicate samples per treatment. GUS activity was measured using a Labsystem Fluoroskan II spectrophotometer and is presented both in absolute activity (Act) and as a percentage of 35S:GUS activity (%35S).

constructs are represented as “promoter:reporter gene”.

For example, “35S:GUS” is the 35S promoter and the GUS reporter gene. “S5nc” and “S7nc” are the promoters for segments 5 and 7, respectively of SCSV.

TABLE 4

SCSV promoter directed GUS activity in tobacco protoplasts

Treatments	GUS Activities				
	Expt 1		Expt 2		Average
	Act	% 35S	Act	% 35S	% 35S
No DNA	13.8	0%	10.5	0%	0%
35S:GUS	113	100%	117	100%	100%
S5nc:GUS	52.3	39%	61	48%	44%
S7nc:GUS	93	80%	106	90%	85%

All experiments were done using duplicate samples per treatment. GUS activity was measured using a Labsystem Fluoroskan II spectrophotometer and is presented both in absolute activity (Act) and as a percentage of 35S:GUS activity (%35S).

40

45

50

55

60

65

TABLE 5

Promoter activities (GUS expression levels) of deletion derivatives of segment 5 and 7 non-coding regions in protoplasts. Levels are expressed as percentages of the activity of the respective full-length non-coding sequence.

Promoter	Deletion ^a	GUS Activity			
		Tobacco		Subclover	
		Expt 1	Expt 2	Expt 1	Expt 2
Segment 5	dNde	101	110	—	—
	dPml (stem-loop)	65	88	—	—
	dAfl (Stem-loop + common region)	70	102	63	91
Segment 7	dPst	5	18	6	4
	dAfl (stem-loop + common region)	50	55	67	39

^aSee FIG. 4 for maps of deletion derivatives.

TABLE 6

Transactivation of segment 5 promoter activity (GUS expression) in tobacco and subterranean clover protoplasts by gene product of segment 2.

Promoter Construct	Protoplasts	GUS Activity			
		Expt 1	Expt 2	Expt 3	Expt 4
S5nc:GUS	Tobacco	100	100	—	—
S5nc:GUS + 35S:Seg 2 RAP	Tobacco	262	217	—	—
S5nc:GUS	Subclover	100	100	100	100
S5nc:GUS + 35S:Seg 2 RAP	Subclover	132	176	188	770
S5nc:GUS + Seg 2 dimer ^b	Subclover	—	—	—	320

^aGUS activities are expressed as percentages of the S5nc:GUS construct in each experiment

^bSee Example 9

TABLE 7

Relative GUS activity in leaf extracts of independent transgenic tobacco plants containing different promoter:GUS constructs as determined by fluorometric assays ^a		
Promoter	GUS Activity	Average
Non transgenic control	123	
	Average	123
35S	#3	38,431
	#6	20,052
	#8	20,648
	#11	28,325
	#12	24,700
	Average	26,431
S4nc	#1	7,229
	#2	4,690
	#5B	4,300
	#9	6,218
	#18	4,895
	#19	6,098
	Average	5,572
S7nc	#4	642
	Average	642

^aGUS activity presented is the best 25% of the transgenic plants tested.

EXAMPLE 11

Further Characterisation of SCSV Promoter Activities in Transgenic Plants

Transgenic plants of tobacco transformed with the five (Segments 1, 3, 4, 5 and 7) SCSV promoter:GUS fusion cassettes were assayed for GUS activity by both histochemical (FIGS. 8 and 9) and fluorometric assays (FIG. 10). Samples taken from tissue-cultured and young glasshouse-grown plants produced the same GUS expression pattern. GUS activity was observed in all plant parts, including roots, stems, leaves, petioles and all flower parts. Promoter 5 construct gave relative lower GUS expression in pollen than other promoters. The results from fluorometric assays confirmed previous data showing that segment 4 promoter was the highest expressor, with activity 10-fold or greater than the rest (FIG. 10), but is still lower than that of the 35S promoter. The expression levels of the segment 1, 3, 5 and 7 promoters were comparable to those of the phloem-specific promoter roIC in tobacco (Schmulling et al., 1989; Sugaya et al., 1989). Plants transformed with the promoterless GUS construct did not express GUS by either assay method. Histochemical assays showed that expression of all promoter constructs was the highest in vascular tissues, with high expressors being more constitutive than low expressors which are more vascular-limited (FIG. 8). In general, promoter 1, 3, 5 and 7 constructs are expressed mostly in the vascular tissues. In particular, GUS expression by promoter 1 and 3 constructs are mainly restricted to phloem tissues. However, for all promoters histochemical staining of leaves showed that GUS expression in these tissues are often blotchy (constitutive and vascular-limited) and variable between leaves of the same plant. Dark field microscopy (Jacobsen-Lyon et al., 1995) also showed that none are strictly vascular-limited (FIG. 9).

Twenty primary transgenic subterranean clover plants expressing the seg 7 promoter:GUS gene were further characterised by histochemical assays (Table 9). These assays showed that GUS activity was observed in all plant parts, including roots, stems, leaves and petioles. GUS expression was the highest in vascular tissues, with some leaves being more constitutive and blotchy than other organs

and high GUS expressing plants being more constitutive than low expressing ones. Samples taken from tissue-cultured and glasshouse-grown plants produced the same GUS expression pattern.

EXAMPLE 12

Detection of Promoter Activity in SCSV Segment 2 DNA

Experiments showed that the non-coding regions from the SCSV segments 2 and 6 DNAs were unable to drive the expression of GUS gene in transgenic tobacco. These regions are only 179 and 159 nucleotides long, respectively, and it is likely that additional sequences are required for promoter activity. To test this hypothesis, a new segment 2 promoter sequence was constructed consisting of the DNA fragment from nucleotides 526 to 46 and fused to the promoterless GUS vector pKGO (FIG. 11). The fusion construct was electroporated into tobacco protoplasts. GUS activity was detected in electroporated tobacco protoplasts at levels similar to that of segment 5 promoter:GUS construct (Table 10).

A binary vector containing the above SRnc promoter:GUS fusion DNA was also transformed into tobacco plants as described in Example 4. Histochemical staining of several transformed tobacco plants showed that GUS expression was mainly vascular. These results showed that additional sequence from the SCSV segment 2 DNA coding region is necessary for promoter function. Since the SCSV segment 6 is a variant of the segment 2, it is expected that a similar construct comprising the noncoding and part of the coding region of this DNA will produce an active promoter. Thus, all SCSV promoters are expected to be suitable for driving gene expression in plants.

EXAMPLE 13

Enhancement of Gene Expression by SCSV Transcription Termination and Polyadenylation Signals

Effective gene expression requires not only a promoter, but also specific nucleotide sequences at the 3' end of the coding region of the gene, known as the termination and polyadenylation signals (Messing et al., 1983; Joshi 1987b; Gil and Proudfoot, 1984; Rothnie et al., 1994). These special sequences are required to signal the RNA polymerase to stop transcription and to allow further processing of the RNA transcript. The activity of the termination and polyadenylation signals may affect the transcription efficiency and stability of the RNA being transcribed. Some widely used termination/polyadenylation sequences include those from the NOS aepicker et al., 1982), OCS (Janssen and Gardner, 1989) and CaMV 35S (Pietrzak et al., 1986) genes.

Each of the SCSV DNA segment (or component) contained a terminator sequence comprising a termination and a polyadenylation signal sequence in the noncoding region (Table 11). To demonstrate activity of the termination/polyadenylation signals in SCSV DNA, GUS expression vectors containing either the segment 3 or segment 5 polyadenylation and termination signal (FIG. 12) was constructed and subjected to transient expression in tobacco protoplasts. The respective terminator sequence was amplified by PCR with several restriction sites incorporated into the primers (FIG. 12). The amplified terminator fragments were cut with the indicated restriction enzymes and cloned into the pKGO recombinant plasmid containing either S1nc

or S4nc promoter:GUS:OCS3' constructs, from which the OCS3' sequence has been deleted (FIG. 12). The resultant S1nc:GUS:SC3Tr (the segment 1 promoter here carries a deletion of the HindIII fragment from nucleotides 641-782 which has no effect on GUS activity) and S4nc:GUS:S5Tr constructs were electroporated into tobacco protoplasts and assayed for GUS activity. The results showed that GUS activity was increased 2 to 3-fold when the SCSV termination/polyadenylation sequence was used instead of the commonly used OCS termination/polyadenylation sequence in the same construct (Table 12). In the same experiment, the construct S1nc:GUS:S3Tr produced over two-fold higher activity than the 35S:GUS:OCS3' construct (Table 12). These results indicate that each of the SCSV DNA components contains a different termination and polyadenylation signal sequence which can be used in various combination with the SCSV promoters to regulate and/or enhance expression of foreign genes in plants. As with the SCSV promoter sequences, the SCSV termination/polyadenylation sequences are advantageous over currently available termination/polyadenylation sequences by their small sizes (160-170 nucleotides) and the availability of a broad range of transcription regulators with different strengths and tissue specificities for genetic manipulation. The results also show that the use of a SCSV promoter in combination with a SCSV terminator sequence in higher levels of gene expression than constructs using the 35S promoter in conjunction with one of the common transcription terminator sequences.

EXAMPLE 14

Activity of SCSV Promoters in Transgenic Potato Plants

pGA470 binary vector containing the S4nc:GUS:NOS fusion construct cloned in pHW9 (FIG. 3) was used to transform potato plants. pHW9 is derived from pHW8 (Dolferus et al., 1994) into which the polylinker from pGEM3zf(+) is inserted. The recombinant binary vector was transformed into *Agrobacterium tumefaciens* strain LBA4404 by electroporation (Nagel et al., 1990). Potato cultivars Atlantic and Sebago were transformed and regenerated essentially as described by Wenzler et al. (1989) except for the following modifications. Stem pieces instead of leaf pieces were used for transformation and 10 mg/l of benzylaminopurine (BAP) instead of 2.24 mg/l was used during co-cultivation. After co-cultivation, stage 1 medium is supplemented with 100 mg/l of cefotaxime and not kanamycin or carbenicillin. Stage II medium contained 2 mg/l BAP, 5 mg/l GA3, 100 mg/l kanamycin and 100 mg/l cefotaxime.

Six transformed plants comprising 5 of cultivar Atlantic and 1 of cultivar Sebago were transferred and grown in the glasshouse for 10-11 weeks until small tubers formed. Tissues from different parts of the plants were assayed by histochemical GUS staining. The results showed that GUS was highly expressed in all plant parts including roots, stolons, tubers, stems and leaves but the expression was predominantly vascular, including cambium, phloem elements and some xylem elements (FIG. 13). As in other transgenic hosts, GUS expression in non-vascular tissues of highly GUS active plant materials, especially young tubers, was more evident than in less active tissues when compared with plants transformed with a 35S:GUS:NOS construct, SCSV promoter directed GUS expression in tubers was at least as high as that of the 35S:GUS construct.

EXAMPLE 15

Activity of SCSV Segment 7 Promoter in Transgenic Cotton Plants

pGA470 binary vector containing S7nc:GUS:NOS fusion construct cloned in pHW9 was used to transform cotton

plants. The recombinant binary vector was transformed into *Agrobacterium tumefaciens* strain AGL1 by triparental mating. Cotton (*Gossypium hirsutum*) cv. coker 315 was transformed and regenerated as described by Cousins et al. (1991).

Transformed plants were grown in the glasshouse and leaf tissues from 18 independent transgenic plants were assayed for GUS activity by histochemical staining. GUS activity varied between plants. Five of these plants showed strong GUS expression, similar in range to 35S promoter driven GUS expression and was predominantly in the vascular tissues (FIG. 14). GUS activity was especially strong in the gossypol glands. As in other transgenic hosts, GUS staining in highly expressed tissues were also constitutive.

A variety of tissues from these plants were then stained and vascular expression was observed in all organs including roots, stems, petioles, petals and other vascularised floral parts. Expression appears to be particularly high in young flower buds. Seedlings from one of the lines was screened for GUS activity. All 10 progenies stained heavily in roots and leaves indicating that the gene was inherited and that the line probably contained more than one independent insertion site.

EXAMPLE 16

Stability of Transformed SCSV Promoter: GUS Expression Cassette in Transgenic Plants

The stability of GUS expression driven by the various SCSV promoters in transgenic tobacco and subclover were further characterised in T1 generation seedlings of subterranean clover and tobacco plants.

In tobacco, T1 seedlings from 10 independent transgenic lines were assayed by histochemical staining. The results showed that the expression of the GUS gene driven by all the five (segments 1,3,4,5 and 7) promoters was stable in the T1 seedlings, with the pattern of expression being maintained in all cases between T0 and T1 plant tissues of the same age. In very young stems where the vascular tissues are not well differentiated, expression from all promoters were very high and was detected through out the stem tissues. Gradual vascular limitation occurs with age and with increasing differentiation of the vascular bundles. As with T0 plants, the segment 4 promoter mediated GUS expression was more constitutive than others.

Fifty 2-3 month old T1 seedlings from 15 independent transgenic subclover plants expressing the S7nc:GUS fusion construct were assayed for GUS activity by histochemical and fluorometric assays. The results showed that the expression of the GUS gene driven by the segment 7 promoter was stable in T1 seedlings, with the pattern of expression being maintained between T0 and T1 plant tissues of the same age. GUS expression was found to generally segregate at the expected ratio of 3:1. The preliminary results from fluorometric assays confirmed the histochemical data suggesting that this segment 7 promoter construct had GUS activity somewhat lower than that of the 35S promoter in leaves and petioles (Table 13). GUS activity in subterranean clover stems, however, was 3-fold higher than in petioles and 6fold higher than in leaves (Table 14). The age of the plants at the time of assay was 2 to 3 months.

EXAMPLE 17

Transient Activity of SCSV Promoter in Soybean Leaves

The SCSV promoter:GUSconstruct used (Table 15) was derived from the promoterless GUS plasmid pKGO (FIG. 4;

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pJKKmf(-) K1W1 GUS:OCS) described previously while the 35S promoter:GUS construct was pGUS. pGUS is derived by cloning the Gus gene from pKIWI101 into the plant expression vector pDH51 (Pietrzak et al., 1986).

For transient GUS expression in soybean tissues, the GUS constructs were introduced into tissues tissues by particle bombardment using the Bio-Rad Biolistic PDS-1000/He Particle Delivery System as above. A 50 μ l suspension containing 3 mg of a 1:1 ratio of 1 and 5 μ gold particles plus 6 μ g of DNA was shot onto plates containing 3 leaves each. Fully expanded leaves used in these experiments were prepared from 24 day old soybean plants cv. Wayne. After particle bombardment, GUS activity was assayed 24 hours later by vacuum infiltration of the leaves with X-Gluc (Craig, 1992).

The results (Table 15) showed that in transient expression in soybean leaves, SCSV segment 4 promoter was more active (25–35 spots/leaf) than the 35S promoter (10–15 spots/leaf) when the respective plasmids were shot into soybean leaves.

EXAMPLE 18

Testing of SCSV Promoters for Callus-specific Expression

All seven SCSV non-coding sequences were cloned into the promoterless GUS vector pHW9. Binary vectors each containing one of the seven SCSV promoter:GUS fusion constructs were transformed into tobacco tissues by *Agrobacterium*-mediated gene transfer. At 2–3 weeks after transformation, calli containing primordia of transformed shoots were subjected to histochemical GUS staining. Best expression was observed in calli transformed with segment 1 followed by the S4nc:GUS:OCS constructs. This result suggests that the segment 1 promoter is best suitable for selectable marker gene expression and that the segment 4 promoter is best for gene expression.

EXAMPLE 19

Characterisation of Regulatory Sequences of the *Flaveria bidentis* MeA Gene

In *Flaveria bidentis* (Chitty et al., 1994) the MeA gene is the gene that codes for the NADP-malic enzyme adapted for C4 photosynthesis. The structure and putative promoter and transcription termination/polyadenylation signal sequences of this gene has been isolated and the terminator sequence determined (FIG. 15). The potential activities of the putative promoter element (MeA 5' sequences) and terminator (MeA 3' sequences) of the *F. bidentis* MeA gene were studied in transgenic *F. bidentis* plants using GUS expression vectors (FIG. 16). A long version of the MeA 3' terminator sequence (MeA 3'L=5.5 kb from the stop codon) was used in these experiments. In FIG. 16, the GUS expression cassette ME20 is ligated to the binary vector pGA470 (An et al., 1985) while ME29 is cloned into pGA482 (An, 1986). Plants were transfected with these vectors as described by Chitty et al. (1994)

Study of GUS activity of the transformed plants by histochemical staining and fluorometric assays showed that the MeA 3' sequence of the gene is required for high level expression of GUS in leaves of transgenic *F. bidentis* plants (Table 16). The 5' sequences of the gene do not appear to contribute to gene expression in leaves but appear to direct expression in meristems and stems in the presence of a suitable transcription termination/polyadenylation signal sequence such as the OCS 3' (Table 16).

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EXAMPLE 20

Use of the MeA 3' Termination/polyadenylation Signal Sequences in SCSV Promoter Constructs to Enhance Gene Expression in Monocotyledonous Plants

Because most gene control elements are located at the 5' end, the activity of the MeA 3' sequence is tested in conjunction with the S4nc SCSV promoter with the view to enhance gene expression directed by the SCSV promoters. For these experiments, a short version of the MeA 3' terminator sequence was used (MeA 3'S; 900 bases from the stop codon) to prepare GUS expression vectors containing the S4nc promoter with either the OCS 3', SCSV segment 5 3' (SC5Tr) or the MeA 3' transcription termination/polyadenylation signal sequence. These constructs were derived from the promoterless GUS plasmid pKGO described previously and the recombinant plasmid pBS237 containing the S4nc:GUS:MeA3' construct is presented in FIG. 17. GUS activity conferred by these constructs were assayed in Japonica rice callus cv. Taipei 309. The constructs were introduced into rice calli by particle bombardment using the Bio-Rad Biolistic PDS-1000/He Particle Delivery System (Bio-Rad Laboratories) and compared with results obtained in dicotyledonous tissues such as soybean leaves and tobacco protoplasts (Table 17). For rice particle bombardment experiments, 4 mg of a 1:1 ratio of 1 and 5 micron gold particles plus 5 μ g of DNA in a total of 50 μ l volume was shot onto six plates of calli. The DNA was made up with a 4:1 molar ratio of each of the vectors containing GUS gene to the vector containing the selectable marker gene. The vector containing the selectable marker was pTRA151 (Zheng et al., 1991). Each plate contained 50–100 fresh secondary calli derived from mature embryos. Forty hours after DNA bombardment, GUS activity was detected by placing the calli in 0.3% w/v X-Gluc solution in 100 mM phosphate buffer. Blue spots were counted after overnight incubation.

For transient GUS expression in tobacco and soybean, only the GUS constructs were introduced into protoplasts and leaf tissues, respectively. After electroporation, tobacco protoplasts were assayed for GUS activity as previously described. The constructs were introduced into soybean tissues by particle bombardment as described above.

The results showed that in the monocotyledonous rice tissues, a 16-fold higher activity was obtained with the MeA 3' construct compared to the SCSV terminator (Table 17). In similar experiments, a highly expressed GUS construct containing the ubiquitin promoter:GUS:NOS cassette (Christensen et al., 1992) has about 4-fold higher activity than the SC4:GUS:MeA3' construct.

In the dicotyledonous tissues, similar activities were obtained with both of these constructs in tobacco protoplasts and soybean leaves. However, both were 2-fold higher in activity than that obtained with the OCS terminator in tobacco protoplasts (Table 17).

These results suggest that the MeA3' sequence can be used to enable gene expression directed by SCSV promoters in monocots.

EXAMPLE 21

Use of New Vectors Containing SCSV Promoters and Terminators to Drive a Selectable Marker Gene in Transgenic Plants

The suitability of using SCSV promoters to drive a selectable marker gene as a basis for selecting transgenic

plants after transformation and regeneration was tested in tobacco plants. The selectable marker used is the kanamycin resistance gene, nptII. Binary vectors containing either a SCSV segment 1 (pBS246) (FIG. 18) or a SCSV seg 7 promoter (pKHAN4) (FIG. 19) fused to the nptII gene were constructed from the pART27 (Gleave, 1992) and pKSB-bar1 (FIG. 19), respectively. These were transformed separately into tobacco plants (Ellis et al., 1987) and putative transgenic plants were selected under kanamycin selection using 100 µg/ml kanamycin (FIG. 20). Kanamycin resistance was confirmed in the transgenic plants by dot blot assay for the nptII gene activity (McDonnell et al., 1987) and survival of the transgenic plants under 100 µg/ml kanamycin in a rooting medium. The results showed that the SCSV segment promoter construct produced at least as many kanamycin resistant plants as the 35S promoter construct use in the same experiment and is, therefore, as effective as the 35S promoter for selecting transgenic tobacco plants based on kanamycin resistance (Table 18). Tobacco transformed with pKHAN4 is resistant to 100 µg/ml kanamycin in regeneration medium and 50 µg/ml kanamycin in rooting medium. Restriction maps of pKSB.bar1 and pKHAN2 used to produce pKHAN4 are shown in FIG. 19.

EXAMPLE 22

Development of a New Plant Gene Expression Vector System

A new expression vector comprising a SCSV segment 4 promoter and a SCSV segment 5 terminator driving any useful gene of interest (pICAN 1) (FIG. 21) has been constructed from a pGEM derivative and the resultant expression cassette can be inserted into the binary vectors pBS246 and pKHAN4. The resultant binary vectors can then be used to transform plants of economic importance especially cotton, subclover, potato and white clover under kanamycin selection. Other binary vectors can be constructed from different combinations of SCSV promoters and terminators to produce a fall range of binary vector system for plant gene expression.

TABLE 9

GUS activity of SCSV segment 7 promoter:GUS construct in primary transgenic subterranean clover plants (To)		
Plant #	Basta Resistance	GUS Activity
1	R	+++
2	R	++
3	R	-
4	R	++
5	S	++
6	R	-
7	R	++++
8	R	++++
9	MR	+++
10	R	+++
11	R	+++
12	MR	-
13	MR	++
14	S	++
15	R	+
16	N.d.	++++
17	N.d.	+++
18	N.d.	-
19	N.d.	+++
20	N.d.	++

Plants were analysed two months after transfer of plants to glasshouse from tissue culture.
 Basta (phosphinothricin - [PPT] resistance was assayed by painting basta at 1 gm
 PPT/litre onto fully unfolded young leaves and reaction was assayed after one week.
 R No damage;
 MR Moderate damage to leaflet;
 S Leaflet dead
 N.d. Not determined

TABLE 8

Sequences and positions of PCR primers for cloning non-coding regions and corresponding PCR fragment sizes.

Primer 1 Name	Position of 5' end sequence (5'-3')	Primer 1	Primer 2 Name	Position of 5' end sequence (5'-3')	Primer 2	Fragment size (bp)
S1nc3 (SEQ ID NO: 16)	241	GGCGTGCCTCGGCCATGG CGCTATGAAATCTGAAC	S1nc5 (SEQ ID NO:17)	577	GGCGTGCCTCGGGGATCCT ATGTTGTAATTTTATATGG	665
S2nc3 (SEQ ID NO: 18)	79	GGCGTGCCTCGGCCATGG AAGCTTAGAGAGAGAAAAG	s2nc5 (SEQ ID NO:19)	924	GGCGTGCCTCGGGGATCCA ATAAAAGAATATATATTATTTG	177
S4nc3 (SEQ ID NO: 20)	347	CTCACTATAGAACCATGGA CACAAGATTCTAAG	S3nc5 (SEQ ID NO:21)	863	CTCACTAAAGGGGGATCCT GAGATGTAATTGTG	502
S4nc3 (SEQ ID NO: 22)	347	CTCACTATAGAACCATGGA AAGCCAGAACAAAAG	S4nc5 (SEQ ID NO:23)	803	CTCACTAAAGGGGGATCCT AATTGTTATTATCA	546
S5nc3 (SEQ ID NO: 24)	372	CTCACTATAGAACCATGG TCGTTGTAAATGAC	S5nc5 (SEQ ID NO:25)	874	CTCACTAAAGGGGGATCCT AATTGTGATGATT	523
S6nc3 (SEQ ID NO: 26)	50	CTCACTATAGAACCATGG TGGCCAGGGAAGCGA	S6nc5 (SEQ ID NO:27)	903	CTCACTAAAGGGGGATCCT GAAAACCTGCGAA	164
S7nc3 (SEQ ID NO: 28)	383	CTCACTATAGAACCATGG CTTAAACCAGAACA	S7nc5 (SEQ ID NO:29)	817	CTCACTAAAGGGGGATCCT AATTAATAGTAATTATG	554

TABLE 10

GUS activity in tobacco protoplasts directed by SCSV segment 2 promoter to tobacco protoplasts relative to the 35S promoter			
Construct	GUS Activity		
	Experiment		
	1	2	
S2nc:GUS:OCS3'	0.46	0.45	
35S:GUS:OCS3'	1	1	

TABLE 11

Putative Polyadenylation and Termination signals in SCSV DNA Components	
DNA Component	Putative Polyadenylation/Termination Signals
Seg. 1	AATTAT ^a -(N) ₁₉ -TGTGTTTT ^c
Seg. 2	AATAAA ^b -(N) ₁₀ -TTGTTTT ^d
Seg. 3	AATAAA ^b -(N) ₃ -TTGTT ^e
Seg. 4	AATAAA ^b -(N) ₈ -TTATTGTT ^f
Seg. 5	AATAAA ^b -(N) ₃ -TTGTTTT ^d
Seg. 6	AATAAA ^b -(N) ₉ -TTGTT ^e
Seg. 7	AATAAA ^b -(N) ₁₁ -TTGTTTT ^g

N, any nucleotide residue, wherein numbers refer to the number of residues in the sequence

^aSEQ ID NO: 14

^bSEQ ID NO: 15

^cSEQ ID NO: 30

^dSEQ ID NO: 31

^eSEQ ID NO: 32

^fSEQ ID NO: 33

^gSEQ ID NO: 34

TABLE 12

GUS Activity Directed by SCSV Promoter in the presence of different terminators in tobacco protoplasts				
	GUS ACTIVITY			
	Expt 1	Expt 2	Expt 3	Av
S4nc:GUS:OCS3'	551	166.3	—	358
S4nc:GUS:SC5Tr	1258	311.8	—	785
No DNA	0	0	0	0
S1nc:GUS:OCS3'	—	—	26	26
S1nc [ΔHindIII] ^h :GUS:OCS3'	—	—	29	29
S1nc [ΔHindIII]:GUS:SC3Tr	—	—	84	84
35S:GUS:OCS3'	—	—	35	35

In each experiment, duplicate electroporations of each construct was performed.

Results are the average of the duplicates.

^hContains a deletion of a HindIII fragment.

TABLE 13

Fluorometric GUS Assay of Independent T1 generation of transgenic subterranean clover plants expressing either the S7nc:GUS or the 35S:GUS Construct			
Construct/Plant #	Leaf (Young)	Petiole (Young)	
	[unfolded]	[unfolded]	
S7nc:GUS Plant #1	56.6	120	
S7nc:GUS Plant #2	35	48	
S7nc:GUS Plant #3	116	140	
35S:GUS Plant #1	120	238	
35S:GUS Plant #2	280	238	

Plants were 2-3 months old when assayed.

Results show differential expression in different tissues.

TABLE 14

Distribution of GUS activity in a T1 generation transgenic subterranean clover plant expressing the S7nc:GUS construct			
Source of Tissue	Leaf	Petiole	Stem
Top-[folded leaf; #1 leaf position]	1	1.9	2.0
Middle [#3 leaf position]	1.6	5.8	22.0
Bottom [#17 leaf position]	4.0	4.8	12.6

Plants were 2-3 months old when assayed.

Results show differential expression in different tissues.

TABLE 15

Transient expression of GUS in soybean leaves directed by a SCSV promoter		
Constructs	GUS Expression in soybean leaves* (# spots/leaf)	
S4nc:GUS:SC5Tr	25-35	
35S:GUS:35STr	10-15	

*Results from one experiment in which spots from 3 leaves were counted in each treatment

TABLE 16

Characterisation of GUS activity directed by MeA 3'L sequence (5.5 kb version) in Transgenic <i>Flaveria bidentis</i> Plants	
Constructs	GUS Expression
MeA:GUS:MeA 3'L (ME24)	High GUS in leaves High GUS in meristem Moderate GUS in stems
MeA:GUS:OCS 3'(ME20)	No GUS in leaves High GUS in meristem Moderate GUS in stems

TABLE 17

Transient expression of GUS in rice callus, soybean leaves and tobacco protoplasts showing enhancement of SCSV promoter activity by MeA 3's sequences in rice callus			
Constructs	GUS Expression		
	Rice callus (Rel # spots)	Soybean leaves (Rel # spots)*	Tobacco protoplasts (Fluorescence)
S4nc:GUS:OCS3'	ND ^a	ND	0.49
S4nc:GUS:SC5Tr	0.06	1	1.0
S4nc:GUS:MeA 3'S	1	1	1.1

ND Not done

*Average number of spots from 3 leaves in one experiment

TABLE 18

Selection of putative transgenic tobacco plants transformed with Kanamycin resistance gene driven by 35S or S4nc promoter.			
Selection Criteria	Constructs	% Kanamycin resistant	
npt II dot Blot	35S:npt II:35STr	(1/3)*	33%
	S1nc:npt II:SC3Tr	(7/16)	43%
Kanamycin selection in rooting medium	35S:npt II:35STr	(10/21)	48%
	S1nc:npt II:SC3Tr	(11/21)	52%

*Number of resistant plants in total number of plants tested.

TABLE 19

Summary of the activities of SCSV transcription regulatory elements in plant tissues			
SCSV promoter	Gene Expressed	Protoplasts	Activity Detected Transgenic Plants
A.			
Seg 1	GUS, nptII	Tobacco	Tobacco
Seg 2	GUS	Tobacco	Tobacco
Seg 3	GUS	Not done	Tobacco
Seg 4	GUS	Tobacco	Tobacco, potato
Seg 5	GUS	Tobacco, subclover	Tobacco
Seg 6	None	Not done	Not done*
Seg 7	GUS, nptII	Tobacco, subclover	Tobacco, subclover, cotton
B.			
SC3Tr	GUS, nptII	Tobacco	Tobacco
SC5Tr	GUS	Tobacco	Not done

*Sequence used probably insufficient to be active. Additional DNA sequence may be required as shown in segment 2.

BIBLIOGRAPHY

An, G. (1986). Development of plant promoter expression vectors and their use for analysis of differential activity of nopaline synthase promoter in transformed cells. *Plant Physiol.* 81, 86-91.

An, G., Watson, B. D., Stachel, S., Gordon, M. P. and Nester, E. W. (1985). New cloning vehicles for transformation of higher plants. *EMBO J.* 4, 277-284.

Benfey, P. N. and Chua, N.-H. (1990). The cauliflower mosaic virus 35S promoter: combinatorial regulation of transcription in plants. *Science* 250, 959-966.

Burns, T. M., Harding, R. M., Hafner, G., Beetham, P. and Dale, J. L. (1993). Single-stranded DNA genome organisa-

tion of banana bunchy top virus. IXth International Congress of Virology, Glasgow, Abstract W62-8.

Chitty, J. A., Burbank, R. T., Marchall, J. S., Chen, Z. and Taylor, W. C., Genetic Transformation of the C⁴ Plant, *Flaveria bidentis*, *The Plant Journal* 6: 949-956, 1994.

Chu, P., Boevink, P., Surin, B., Larkin, P., Keese, P and Waterhouse, P. (1994). Non-germinated single stranded DNA plant viruses. In "Pathogenesis and host-parasite specificity in plant diseases: Vol III. Viruses and Viroids". Pergamon Press.

Chu, P. W. G. and Helms, K. (1988). Novel virus-like particles containing circular single-stranded DNA associated with subterranean clover stunt disease. *Virology* 167, 38-49.

Chu, P. W. G., Keese, P., Qiu, B. S., Waterhouse, P. M. and Gerlach, W. L. (1993a). Putative full-length clones of the genomic DNA segments of subterranean clover stunt virus and identification of the segment coding for the viral coat protein. *Virus Research* 27, 161-171.

Chu, P. W. G., Qiu, B. S., Li., Z-y and Larkin, P. (1993b). Replication of subterranean clover stunt virus in pea and subterranean clover protoplasts. *Virus Research* 27, 173-183.

Christensen, A. H., Sharrock, R. A. and Quail, P. H. (1992). Maize polyubiquitin genes: structure, thermal perturbation of expression and transcript splicing, and promoter activity following transfer to protoplasts by electroporation. *Plant Mol. Biol.* 18, 675-689.

Cousin, Y. L., Lyons, B. R. and Llewellyn, D. J. (1991). Transformation of an Australian cotton cultivar: prospects for cotton improvement through genetic engineering. *Aus. J. Pl. Physiol.* 18, 481-494.

Craig, S., (1992) The GUS Reporter Gene - Application to light and transmission electron microscopy. In *GUS protocols: using the GUS gene as a reporter of gene expression*. S. R. Gallagher, Ed. Academic Press, Inc., Page 115.

Das, A. (1993). Control of transcription termination by RNA-binding proteins. *Ann. Rev. Biochem.* 62, 893-930.

de Carvalho, F., Gheysen, G., Kushnir, S., Van Montagu, M., Inze, D. and Castresana, C. (1992). Suppression of β -1,3-glucanase transgene expression in homozygous plants. *The EMBO J.* 11, 2595-2602.

Depicker, A., Satchel, S., Dhaese, P., Zambryski, P. and Goodman, H. (1982). Nopaline synthase:transcript mapping and DNA sequence. *J.Mol. Appl. Genet.* 1, 561-575.

Del Sal, G., Manfioletti, G. and Schneider, C. (1989). The CTAB-DNA precipitation method: a common mini-scale preparation of template DNA from pagemids, phages or plasmids suitable for sequencing. *Biotechniques* 7, 514-518.

Devereaux, J., Haerberli, P. and Smithies, O. (1984). A comprehensive set of sequence analysis programs for the VAX. *Nucleic acids Res.* 12, 387-395.

Ditta, G., Stanfield, S., Corbin, D. and Helsinki, D. R. (1980). Broad host range DNA cloning system for gram-negative bacteria: construction of a gene bank of *Rhizobium meliloti*. *Proc. Natl. Acad. Sci. USA* 77, 7347-7351.

Dolferus, R., Jacobs, M., Peacock, J. W., and Dennis, L. S. (1994). Differential interactions of promoter elements in stress responses of the *Arabidopsis Adh* Gene. *Plant Physiol.* 105, 1075-1087.

Ellis, J. G., Llewellyn, D. J., Dennis, E. S. and Peacock, W. J. (1987). Maize *Adh-1* promoter sequences control anaerobic regulation: addition of upstream promoter elements from constitutive genes is necessary for expression in tobacco. *EMBO J.* 6, 11-16.

- Gil, A. and Proudfoot, N. J. (1984). *Nature* 312, 473–474.
- Gil, A. and Proudfoot, N. J. (1984). A sequence downstream of AAUAAA is required for rabbit β -globin mRNA 3'-end formation.
- Gleave, A. P. (1992). A versatile binary vector system with a T-DNA organisational structure conducive to efficient integration of cloned DNA into the plant genome. *Plant Molecular Biology* 20, 1203–1207.
- Harding, R. M., Bums, T. M. and Dale, J. L. (1991). Virus-like particles associated with banana bunchy top disease contain small single-stranded DNA. *J. Gen. Virol.* 72, 225–230.
- Harding, R. M., Burn, T. M., Hafier, G., Dietzgen, R. G. and Dale, J. L. (1993). Nucleotide sequence of one component of the banana bunchy top virus genome contains a putative replicase gene. *J. Gen. Virology* 74, 323–328.
- Hatch, M. D. (1987) C4 photosynthesis: A unique blend of modified biochemistry, anatomy and ultrastructure. *Biochim. Biophys. Acta* 895:81–106.
- Higgins, T. J. V. and Spencer, D. (1991). The expression of a chimeric cauliflower mosaic virus (CaMV) 35S-*pea vicilin* gene in tobacco. *Plant Sci.* 74, 89–98.
- Hoekema, A., Hirsch, P. R., Hooykaas, P. J. J. and Schilperoot, R. A. (1983). A binary plant vector strategy based on separation of *vir*- and *T*-region of the *Agrobacterium tumefaciens* Ti-plasmid. *Nature* 303, 179–180.
- Isogai, M., Sano, Y. and Kojima, M. (1992). Identification of the unique DNA species in the milk vetch dwarf virus-infected leaves. *Ann. Phytopath. Soc. Japan* 58, 631–632, Abstract.
- Jacobsen-Lyon, K. Jesen, E. O., Jorgensen, J. E., Marcker, K. A., Peacock, W. J. and Dennis, E. S. (1995). Symbiotic and nonsymbiotic hemoglobin genes of *Casurina glauca*. *Plant Cell* 7,213–223.
- Janssen, B. J. and Gardner, R. C. (1989). Localised transient expression of GUS in leaf discs following co-cultivation with *Agrobacterium*. *Plant Mol. Biol.* 14, 61–72.
- Jefferson, R. A., Kavanagh, T. A. and Bevan, M. W. (1987). GUS fusions: β -glucuronidase as a sensitive and versatile gene fusion marker in higher plants. *EMBO J.* 6, 3901–3907.
- Joshi, C. P. (1987). Putative polyadenylation signals in nuclear genes of higher plants: a compilation and analysis. *Nucleic Acids Research.* 15, 9627–9640.
- Katul, L., Vetten, H. J., Maiss, E., Makkouk, K. M. Lesemann, D.-E. and Casper, R. (1993). Characterisation and serology of virus-like particles associated with faba bean necrotic yellows. *Ann. Appl. Biol.* 123, 629–647.
- Khan, M. R. I., Tabe, L. M., Heath, L. C., Spencer, D. and Higgins, T. J. V. (1994). *Agrobacterium*-mediated transformation of subterranean clover (*Trifolium subterraneum* L.). *Plant Physiol* 105, 81–88.
- Kirschman, J. A. and Cramer, J. H. (1988). Two new tools: multi-purpose cloning vectors carry kanamycin or spectinomycin/streptomycin resistance markers. *Gene* 58, 163–165.
- Last, D. I., Brettell, R. I. S., Chaudhury, A. M., Chamberlain, D. A., Larkin, P. J., Marsh, E. L., Peacock, J. W. and Dennis, E. S. (1991). pEmu: an improved promoter for gene expression in cereal cells. *Theor Appl Genet* 81, 581–588.
- Lazo, G. R., Stein, P. A. and Ludwig, R. A. (1991). ADNA transformation-competent *Arabidopsis* genomic library in *Agrobacterium*. *Biotechnol.* 9, 963–967.

- Linn, F., Heidmann, I., Siedler, H. and Meyer, P. (1990). Epigenetic changes in the expression of the maize Z1 gene in *Petunia hybrida*: Role of numbers of integrated gene copies and state of methylation. *Mol. Gen. Genet.* 222, 329–336.
- McDonnell, R. E., Clark, R. D., Smith, W. A. and Hinchey, M. A. (1987). A simplified method for the detection of neomycin phosphotransferase II activity in transformed plant tissues. *Plant Mol. Biol. Rep.* 5, 380–386.
- Matzke, M. A. and Matzke, A. J. M. (1991). Differential inactivation and methylation of a transgene in plants by two suppressor loci containing homologous sequences. *Plant Mol. Biol.* 16, 821–830.
- Messing, J., Geraghty, D., Heidecker, G., Hu, N-T., Kridl, J. and Rubenstein, I. (1983). Plant gene structure. In: "Genetic engineering of plants. An agricultural perspective." Kosuge, T., Meredith, C. P. and Hollaender, A. (eds). Plenum Press, New York. pp 211–277.
- Nagel, R., Elliot, A., Masel, A., Birch., R. G. and Manners, J. M. (1990). Electroporation of binary Ti plasmid vector into *Agrobacterium tumefaciens* and *Agrobacterium rhizogenes*. *FEMS Microbiology Letters* 67, 325–328.
- Odell, J. T., Nagy, F. and Chua, N.-H. (1985). Identification of DNA sequences required for activity of cauliflower mosaic virus 35S promoter. *Nature* 313, 810.
- Pietrzak, M., Shillito, R. D., Hohn, T. and Potrykus, I. (1986). Expression in plants of two bacterial antibiotic resistance genes after protoplast transformation with a new plant expression vector. *Nucleic Acids Res.* 14, 5857–5868.
- Richardson, J. P. (1993). Transcription termination. *Critical Review in Biochem. and Mol. Biol.* 28, 1–30.
- Rhode, W., Randles, J. W., Langridge, P. and Hanold, D. (1990). Nucleotide sequence of a circular single-stranded DNA associated with coconut foliar decay virus. *Virology* 176, 648–651.
- Rothnie, H. M., Reid, J. and Hohn, T. (1994). The contribution of AAUAAA and the upstream element UUU-GUA to the efficiency of mRNA 3'-end formation in plants. *EMBO J.* 13, 2200–2210.
- Sambrook, J., Fritsch, E. F. and Maniatis, T. (1989). *Molecular cloning: a laboratory manual*. 2nd ed., Cold Spring Harbor Laboratory Press, New York.
- Sanger, F., Nicklen, S. and Coulson, A. R. (1977). DNA sequencing with chain-terminating inhibitors. *Proc. Natl. Acad. Sci. USA* 74, 5463–5467.
- Sano, Y., Isogai, M., Satoh, S. and Kojima, M. (1993). Small virus-like particles containing single-stranded DNAs associated with milk vetch dwarf disease in Japan. 6th Int. Cong. of Plant Path., Montreal, Canada, Jul. 28–Aug. 6, 1993. Abs. 17.1.27.
- Scheid, O. M., Paszkowski, J. and Potrykus, I. (1991). Reversible inactivation of a transgene in *Arabidopsis thaliana*. *Mol. Gen. Genet.* 228, 104–112.
- Schmulling, T., Schell, J. and Spena, A. (1989). Promoters of the *rolA*, *B*, and *C* genes of *Agrobacterium rhizogenes* are differentially regulated in plants. *Plant Cell* 1, 665–670.
- Sugaya, S., Hayakawa, K., Handa, T. and Uchimiya, H. (1989). Cell-specific expression of the *rolC* gene of the TL-DNA of Ri plasmid in transgenic tobacco plants. *Plant Cell Physiol.* 30, 649–653.
- Taylor, B. H. and Larkin, P. J. (1988). Analysis of electroporation efficiency in plant protoplasts. *Aust. J. Biotech.* 1, 52–57.
- Thomas, J. E. and Dietzgen, R. G. (1991). Purification, characterization and serological detection of virus-like par-

titles associated with banana bunchy top disease in Australia. *J. Gen. Virol.* 72,217-224.

Wenzler, H., Mignery, G., May, G. and Park, W. (1989). A rapid and efficient transformation method for the production of large numbers of transgenic potato plants. *Plant Science* 63, 79-85.

Zheng, Z., Hayashimoto, A., Li, Z. and Murai, N. (1991). Hygromycin resistance gene cassette for vector construction and selection of transformed rice protoplasts. *Plant Physiol.* 97, 832-835.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(iii) NUMBER OF SEQUENCES: 34

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1001 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TAGTATTACC CCCGTGCCGG GATCAGAGAC ATTTGACCAA TAGTTGACTA GTATAATAGC      60
CCTTGGATTA AATGACACGT GGACGCTCAG GATCTGTGAT GCTAGTGAAG CGCTTAAGCT      120
GAACGAATCT GACGGAAGAG CGTTCACACT TAGATCTAGT TAGCGTACTT AGTACGCGTT      180
GTCTTGGGTC TATAAATAGA GTGCTTCTGA ACAGATTGTT CAGAATTTCA TAGCGAGATG      240
GATTCGTGGT ATGGTTACAA TACATACTCA TATGAAGAAG GTGCTGGAGA TGCGAAGAAG      300
GAAGTTTTAT ATAAAATAGG TATTATTATG TTATGTATTG TAGGGATTGT AGTTTTATGG      360
GTTTAAATTA TATTATGTTG TGCTGTTCC TCGTATGCTA AATCAACGAT GGACGCTTGG      420
TTATCTTCGT CTCTATTAT GAAGAGGAAG ATGGCTTCAA GGATTACTGG TACTCCGTTT      480
GAAGAACTG GTCCTCATCG TGAAGAAGA TGGGCTGAAA GAAGAACTGA AGCGACGAAC      540
CAGAATAATA ATGATAATGT AAATAGATTT AGTTGATATG TTGTAATTTT ATATGGATTA      600
ATGAGAATTA TTATTATTCT GTTCTTCGTC TGTGTTTTTT AAGCTTTTTT TGTGTTTTAA      660
TGGCGTCTGG AGAGAGAAA GAATAATTGT AAGGTAGACG ACGATGTAGT GGATTACAGT      720
TGCTTTTACT TCGCCTCGAA GAAAGACACA TTCAAGTTG TGAGTGTAT TGCTTTTGAG      780
GAAGCTTCTT CGAAGCAGCG TATAACTTTA ATTTGAATTT GGTTTTGGCG CGTTAGTGAA      840
ATTGCGGCTG TAAACGTGTC AAGTTGTGAG TGGCTGAAAT AAGATAATAG ATATATTATT      900
ATTGTTTTAA TTAAATCCG CGAAGCGATA TGTTAAGTGA TAAATGAAAC GAAGCGTTTT      960
GATGACGTCA TATGTCTCCG TGCCTACGTC AGCACGGGGC T                               1001

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1022 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

TAGTATTACC CGACCTTGCC ACACCTCCTT GGAACACTTT CTCTCTCTAG AAAGTGTGAG      60
ACTTCTCTCT TCTAAGCTTA TATGGCTAGA AGGTACTGTT TTACATTAAT TTACGCTACT      120

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GAGATAGAGA GAGAACATT CCTCTCCCTC TTCTCTCAAG ACGAATTAAA CTATTTCTGTT	180
GTCGCGCAGC AACTTGCAAC TACTGGACAG AACACCTCC AGGGATTTGT ATCGTTCAAG	240
AACAAAATTC GTCTTGTTGG ATTGAAGAAG AAATTGGTA ATCGAGCTCA CTGGGAAATT	300
GCGAGAGGCA GCGATTCTCA GAATCGCGAT TATTGCTGTA AAGAAACCCT AATTTCTGAA	360
ATTGGGATTC CGGTCATGAA GGGTTCGAAC AAGCGGAAGA CGATGGAGAT TTATGAAGAG	420
GATCCCGAAG AAATGCAATT GAAGGATCCA GATACTGCTC TTCGATGTAA GCGAAGAAA	480
TTGAAAAGAG AATATTGTTT CTGTTATGAT TTTCAGAAAC TCCGTCCATG GCAAATTGAG	540
CTTCACGAGG ATTTAATGGC GGAACAGAT GATCGGAGTA TCATCTGGGT CTATGGTTCA	600
GACGGAGGAG AAGGAAAGAC GAGCTTCGCG AAGGAATTAA TCAGGTATGG ATGGTTTTAT	660
ACAGCCGGAG GGAAGACCCA GGACGTATTA TATATGTATG CTCAAGACCC AGAGAGGAAT	720
ATTGCGTTTG ATGTTCCAGC GTGTTCTTCG GAGATGATGA ACTATCAGGC GATGGAGATG	780
TTGAAGAACA GAGTTTTTGC AAGTACAAAA TATAGGCCTG TAGATCTTTG TATTAGGAAG	840
TTAGTTCATT TAATTGTGTT TGCCAACGTG GCACCTGACC CCACGCGCAT AAGTGAGGAC	900
AGACTTGTA TATCAATTG TTGAATAAAA GAATATATAT TATGTTTTTA ATTTAATTC	960
GCGAAGCGGT AGCCGGTCAT AACACTGTTG CCCTTGGAAC ACTATATATA GCAAGGTCGG	1020
CT	1022

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 991 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAGTATTACC CCCGTGCCGG GATCAGAGAC ATTTGACCAA TAGTTGACTA TGAATAATAG	60
CCCTTGGATT AGATGACACG TGGACGCTCA GGATCTGTGA TGCTAGTGAA GCGCTTAAGC	120
TGAACGAATC TGACGGAAGA GCGGACATAC GCACATGGAT TATGGCCAC ATGTCTAAAG	180
TGTATCTCTT TACAGCTATA TTGATGTGAC GTAAGATGCT TTACTTCGCC TCGAAGTAAA	240
GTAGAAAATT GCTCGCTAAG TTATTCTTTT CTGAAAGAAA TTAATTTAAT TCTAAATTAA	300
ATTAAATGAG TGGCTATAAA TAGATGTTTC GTCTTCGTTG TTTTACAACG AAGCTTAGAA	360
TCTTGTGTTA ATGGCGTTAA GGTATTTCTC TCATCTTCCT GAAGAACTGA AGGAGAAGAT	420
TATGAACGAG CACTTGAAGG AAATTAAGAA GAAGGAATTT CTAGAGAATG TAATTAAGC	480
TGCGTGTGCT GTGTTCAAG GTTTAACAAA GAAGGAGTCT GTTGAAGAAG ACGACATACT	540
ACGCTTCTCT GGGTTTCTGG AAGGTCTGTC TGCATATTAT GCAGAGCGA CGAAGAAGAA	600
GTGTTTAGTT AGATGGAAGA AGAGCGTTGC AATAAATCTG AAATGGAGAG TTATGGAGGA	660
GATGCATTAC AAGCTTTATG GATTTGCAGA CATGGAAGAT TTATATTATT CAGAGTTAGG	720
GTTTCCTAAT TACGGTGAAG ACGATGTAGC TTATCACGAT GGTGCAATTG TAAATGTAA	780
GCAATTAGAA GTTGATTTTG ATGATTTAGG TATTGAGTTT ATGCTATTG TAATTGATAG	840
AGGTTCATAT AAGATAGAAT TATGAGATGT AATTGTGATT AATGAATAAA GAGTTGTTAT	900
TATTCCTTGA ATTACTCCGC GAAGCGGTGT GTTATGTTTT TGTGGAGAC ATATGACGTC	960
ATATGTCTCG CCGACAGGCT GGCACGGGC T	991

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

TAGTATTACC CCGTGCCGGG ATCAGAGACA TTTGACTAAA TGTGACTTG GAATAATAGC      60
CCTTGGATTA GATGACACGT GGACGCTCAG GATCTGTGAT GCTAGTGAAG CGCTTAAGCT      120
GAACGAATCT GACGGAAGAG CGGACAAACG CACATGGACT ATGGCCCACT GCTTTATTAA      180
AGAAGTGAAT GACAGCTGTC TTTGCTTCAA GACGAAGTAA AGAATAGTGG AAAACGCGTA      240
AAGAATAAGC GTAATCAGTA CGCTTCGTGG CTTTATAAAT AGTGCTTCGT CTTATTCCTC      300
GTTGTATCAT CAACGAAGAA GTTAAGCTTT GTTCTGCGTT TTAATGGCGG ACTGGTTTCA      360
CAGTGCCTT AAGACATGTA CTCATGCTCG TGATTTTCA GATATTAAGG CGTCTTCACA      420
ACAGGATTC TTCTGTTGTG ATAGTATGCG AGGTAAATTA TCTGAACCTA GGAAGGTGTT      480
GTTAGTTAGT TGTTTTGTAA GTTTTACTGG TAGTTTTTAT GGAAGTAATA GGAATGTTAG      540
AGGTCAAGTT CAGTGGGTA TGCAGCAAGA TGATGGCGTT GTTCGTCCAA TAGGATATAT      600
TCCTATTGGG GGTATTTTGT ATCATGATGA TTATGGATAT TATCAAGGAG AGAAGACGTT      660
CAATCTGGAC ATCGAGTCAG ATTATCTGAA GCCTGATGAA GATTTTGGG AGAGATTTAC      720
AATTAAATAT GTAATGATA AAGGATTAGA TGATAGGTGT GATGTAATAA GTTATGTAGT      780
TCATACGATG CGTATTAAGG TGTAATTGTT ATTATCAATA AAAGAATTTT TATTGTTATT      840
GTGTTATTTG GTAATTTATG CTTATAAGTA ATTCTATGAT TAATTGTGAA TTAATAAGAC      900
TAATGAGGAT AATAATTGAA TTTGATTAAA TTAACCTGCG GAAGCTATAT GTCTTTCACG      960
TGAGAGTCAC GTGATGTCTC CGCGACAGGC TGGCACGGGG CT                          1002

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 998 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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TAGTATTACC CCGTGCCGGG GTCAGAGACA TTTGACTAAA TATTGACTTG GAATAATAGC      60
CCTTGGATTA GATGACACGT GGACGCTCAG GATCTGTGAT GCTAGTGAAG CGCTTAAGCT      120
GAACGAATCT GACGGAAGAG CGTCATGGTC CACATGTCTA AAGAATAATG CTTTACAGCT      180
GTATTGATTT GACTTTACGC GCTTTACTTT AATTGCTTTA AGTAAAGTAA GATGCTTTAC      240
TTTGCTCGCG ACGAAGCAA GTGATGTGAG CTGCAGAAAT TGATGCTTTA ATTACCGGGT      300
AACACGGTTT GATTGTGGGT ATAAATATGT TCTGTTCGTT TTCTTCGTTG TCATTTTACA      360
ACGAAGATGG TTGCTGTTCC ATGGGAAGA AAGGGTCTGA GGTCTCAAAG GAGAAAATAT      420
TCGCGAATTG CTTACAAACC TCCTTCGTCT AAGGTTGTAA GTCATGTGGA GTCTGTTCTG      480
AATAAGAGAG ATGTTACTGG AGCGGAGGTT AAGCCATTCG CTGATGGTTC AAGGTATAGT      540

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ATGAAGAAGG TAATGTTGAT TGCAACATTA ACTATGGCTC CTGGAGAATT AGTTAATTAT	600
CTTATTGTGA AGAGTAATTC GCCTATTGCG AATTGGAGTT CGTCTTTCAG TAATCCTTCG	660
TTGATGGTGA AAGAGTCTGT TCAAGATACA GTTACGATTG TTGGAGGAGG AAAGCTTGAG	720
TCTTCTGGTA CTGCTGGTAA AGATGTAACT AAGTCTTTTA GGAAGTTTGT TAAGCTGGGT	780
TCAGGTATTA GTCAGACCCA GCATTGTAT TTAATTATTT ATTCCAGTGA TCGCATGAAG	840
ATCACACTGG AGACGAGAAAT GTATATTGAT GTATAATTGT GATGATTAAT GAATAAAGAG	900
TTGTTTTTAT TCTTTGAATT ACTCCGCGAA GCGGTGTGTT ATGTTTTTGT TGGAGACATA	960
TGACGTCATA TGTCTCCGCG ACAGGCTGGC ACGGGGCT	998

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGTATTACC GCACCTCGCT TACCCTCCTC GCTTCCCTGG GCCCACTATG CCTACTAGAC	60
AAAGCACTAG TTGGGTGTTT AACTTAACT TTGAGGGCGA AATTCCTATT TTGCCCTTTA	120
ATGAAAGCGT TCAGTACGCT TGTGGCAGC ATGAGAGAGT GGGACACGAT CATTACAGG	180
GATTTATACA ATTTAAATCC CGCAACACTA CATTGCGTCA GGCTAAGTAT ATTTTAAATG	240
GACTGAATCC TCATCTGGAA ATTGCTAGGG ATGTAGAGAA GGCACAATTG TACGCGATGA	300
AGGAAGATAG TAGAGTAGCT GGTCCCTGGG AGTATGGGTT GTTTATTAAG AGAGGATCGC	360
ATAAGCGTAA GCTGATGGAG AGATTGAAG AAGATGGAGA AGAGATGAAA ATTGCTGATC	420
CCTCTCTCTA TAGGCGTTGT CTATCAAGGA AGATGGCTGA AGAACAACGT TGTTCCTCTG	480
AGTGAATTA TGAATACGC CTTGGCAAG AAGAAGTAT GCATTTGTTA GAGGAAGAAC	540
CAGATTATAG AACGATAATC TGGGTGTATG GACCTGCTGG TAATGAAGGC AAATCTACAT	600
TTGCAAGACA TCTGTCATTG AAAGATGGTT GGGGTTATCT GCCTGGAGGA AAGACACAAG	660
ATATGATGCA TCTTGTGACT GCTGAGCCTA AGAATAATTG GGTATTTGAC ATACCCAGAG	720
TTAGTTCAGA GTATGTGAAT TATGGTGTAA TAGAACAGGT TAAGAATAGG GTAATGGTGA	780
ATACTAAGTA TGAGCCATGT GTAATGCGGG ATGATAATCA TCCTGTTTCA GTAATTGTGT	840
TTGCAAAATG ACTCCAGAT TTGGGAAAAT TAAGTGAAGA TAGAATAAAA TTAATTCGTT	900
GTTGAAAAC CTGCGAAGGC AGAAGTTATA AAAAAAATGT GTTTGAGAG AAGTCCACA	960
TCGGTAGTTC CGGAAACAG GGTGAGGGAA GCGAGCAATA TAAGGCGAGG TGCCTAT	1017

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 988 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TAGTATTACC CCGTGCCGGG ATCAGAGACA TTTGACTAAA TATTGACTTG GAATAATAGC	60
CCTTGGATTA GATGACACGT GGACGCTCAG GATCTGTGAT GCTAGTGAAG CGCTTAAGCT	120

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GAACGAATCT GACGGAAGAG CGGACATACG CACATGGATT ATGGCCCACA TGTCTAAAGT	180
GTATCTCTTT ACAGCTATAT TGATGTGACG TAAGATGCTT TACTTCGCTT CGAAGTAAAG	240
TAGGAAATG CTCGCTAAGT TATTCCTTTC TGAAAGAAAT TAATTTAAT CTAATTAAT	300
TAAATGAGTG GCTATAAATA GTGTCGATGC TGCCTCACAT CGTATTCTTC TTCGCATCGT	360
CTGTCTGGT TTTAAGCGAT GGTCACTTTT AGTTTCTCTG AGATATACGA TGTGAGCGAC	420
GATGTTCTTG TAAGCGATAG CAGAAGAAGT GTAGCTGTTG AGGTCGAAGA GAAGGTTCAA	480
GTGATTAACG TGAAGGTACT GAGGTTGATT GAAGCTGTTG ATGAAGATAG AGTTGGAGTG	540
AAGGTTATGT TTCGCTCTGT TTACAGATAC AGACGAGAAC TGAAGATTAC GTTGTGGGT	600
TGTAAGATGG AGCTATGGAC TTCGTGAAG TCTTCAGGCA AGTATTCAGT TCAATCTTTG	660
TTGCAGAGGA AGCTTAATGG TATATGTGTT AGTAATTACT GTATAGGTAT TGATATGTTT	720
GTAAGTAATG TTAAGAGATT GATTAATAGA TGTAAATGGA TTACATCTGT TCAAGGTGTT	780
AATCTATAT GTTGTGTTGA TCATATGGAC GAAGAGTAAT TAATAGTAAT TATGATTAAT	840
TATGAGATAA GAGTTGTTAT TAATGCTTAT GAGGAATAAA GAATGATTAA TATTGTTTAA	900
TTTTATTTCG GAAGCGGTGT GTTATGTTTT TGTGGAGAC ATCACGTGAC TCTCACGTGA	960
TGTCCTCCGC ACAGGCTGGC ACGGGGCT	988

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 905 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAGTTTAGC GGGGAAAAA GGACAGTTGA TCTGTTGCTG TTTGCAATTT TTTAAAGGGT	60
ATGTTGTCAG ATGCATGTTG TAATGCTTGT TCATCAACAC ATTATATGAC TTGCAGTTGC	120
TGATGATGGA AACTTAAAGC TTAATACTAC TTTTGTGTTAT TCACCTACAA ATACCGGTTG	180
GGTTCTTTGT TTATCAGGAA TGCTCATTGT ATGTAGCTAA AAGCTGGCCG TTTATAGTTT	240
TATTGCCCTA AATCTGGTAC TTTATCCAAA AACTAAATTT GAAAACATCA AATACTTTTT	300
TCAAGAATGA TAAACTCGTA CACTCTCTAG GGTACTCCTG AAATTTAAAT CAAAATCCAA	360
AACCGCTTAG GAAGGAACAT ATGTGATAAG AACTGAAATT TCGATTAAT ATTACAAGAT	420
AGTCGGCCCA ATTCGAGAGG ACTAGTCTCC GATTACAAGG AGTAAATATC TTAATCTTGA	480
TAAACAAAAC ACATATAAAA AACCTAAAAA TATAGGAACA TAATACATAA ACTAAAAGTT	540
GTGGGAACAG TTACAAATCT GCAGTCTCAC TCCCTAAATT TGTGAGTCAC CTTTCACCTC	600
CAAGTTTTCG AATGTTCTCC CACCATTAC TTTCCCTCCA CCCGGATTCC CTCCAATTAA	660
TAGCTGACAC AACCCGTTTT GACCCAACAT TGGGTTGTA TCAATACATC CGGCCCGGAA	720
AATCGACTTG TCCTCAAGTC GAAAGGAGGG GAATTATTGT GCCAAGCAAA AAGCCATTCTG	780
ATTGGAGGTT GATGGATGAT TTCCTTGTGT TTGAAAGCTT CAAAAGATCC GGCCAAATCA	840
GCTTTTAATG CCTCTTGAAC TGTAGCCACA ACACCACTTT GAAACCTCAA ATCTGTTTTG	900
AATTC	905

(2) INFORMATION FOR SEQ ID NO:9:

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-
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
- TATAAAT 7
- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
- TATATAT 7
- (2) INFORMATION FOR SEQ ID NO:11:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
- AATATAA 7
- (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
- TGA 3
- (2) INFORMATION FOR SEQ ID NO:13:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
- TAA 3
- (2) INFORMATION FOR SEQ ID NO:14:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

-continued

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AATTAT 6

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AATAAA 6

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCGTGCGTC GGCCATGGCG CTATGAAATT CTGAAC 36

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGCGTGCGTC GGGGATCCTA TGTTGTAATT TTATATGG 38

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCGTGCGTC GGCCATGGAA GCTTAGAGAG AGAAAG 36

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

-continued

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
GGCGTGCGTC GGGGATCCAA TAAAAGAATA TATATTATTG 40

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
CTCACTATAG AACCATGGAC ACAAGATTCT AAG 33

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
CTCACTAAAG GGGGATCCTG AGATGTAATT GTG 33

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
CTCACTATAG AACCATGGAA ACGCAGAACA AAG 33

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
CTCACTAAAG GGGGATCCTA ATTGTTATTA TCA 33

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
CTCACTATAG AACCATGGTC GTTGTAAAT GAC 33

-continued

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTCACTAAAG GGGGATCCTA ATTGTGATGA TT

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(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTCACTATAG AACCATGGTG GGCCAGGGA AGCGA

35

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTCACTAAAG GGGGATCCTG AAAACTCTGC GAA

33

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CTCACTATAG AACCATGGCT TAAAACCAGA ACA

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(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTCACTAAAG GGGGATCCTA ATTAATAGTA ATTATG

36

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:

-continued

(A) LENGTH: 8 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
TGTGTTTT	8
(2) INFORMATION FOR SEQ ID NO:31:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 7 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
TTGTTTT	7
(2) INFORMATION FOR SEQ ID NO:32:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 5 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
TTGTT	5
(2) INFORMATION FOR SEQ ID NO:33:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 8 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
TTATTGTT	8
(2) INFORMATION FOR SEQ ID NO:34:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 6 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:	
TTGTTT	6

What is claimed is:

1. A genetic construct comprising an isolated nanovirus promoter from a multicomponent nanovirus, wherein said nanovirus comprises a multicomponent DNA genome, and wherein said nanovirus promoter is operable in a plant cell

and is obtained from a segment of the subterranean clover stunt virus (SCSV) aenome selected from the (roup consisting of:

- (i) SCSV segment 1 (SEO ID NO: 1);
- (ii) SCSV segment 3 (SEO ID NO: 3);

- (iii) SCSV segment 4 (SEO ID NO: 4);
 (iv) SCSV segment 5 (SEO ID NO: 5);
 (v) SCSV segment 7 (SEO ID NO: 7);
 (vi) a nucleotide sequence complementary to any one of (i) to (v); and
 (vii) a fragment of any one of (i) to (vi) which is operable in a plant cell.
2. The genetic construct according to claim 1 wherein the nanovirus genome comprises at least two DNA components or segments.
3. The genetic construct according to claim 1 further comprising a termination and/or polyadenylation sequence wherein said sequence is operably linked to a gene when said gene is operably linked to said promoter.
4. The genetic construct according to claim 3 wherein said termination and/or polyadenylation sequence is of SCSV origin.
5. The genetic construct according to claim 3 wherein said termination and/or polyadenylation sequence is obtained from an SCSV segment selected from the group consisting of: SCSV segment 1 (SEQ ID NO:1); SCSV segment 3 (SEQ ID NO:3); SCSV segment 4 (SEQ ID NO:4); SCSV segment 5 (SEQ ID NO:5); SCSV segment 7 (SEQ ID NO:7); and a transcription termination competent or polyadenylation competent fragment of any one of SEQ ID NOS: 1, 3-5 or 7.
6. The genetic construct according to claim 3 wherein said termination and/or polyadenylation sequence is obtained from the *Flaveria bidentis* MeA gene.
7. The genetic construct according to claim 1 further comprising a heterologous gene operably linked to said promoter.
8. The genetic construct according to claim 3 further comprising a heterologous gene operably linked to said promoter and to said termination and/or polyadenylation sequence.
9. The genetic construct according to claim 4 further comprising a heterologous gene operably linked to said promoter and to said termination and/or polyadenylation sequence.
10. The genetic construct according to claim 7 wherein said heterologous gene is selected from the group consisting of:
- a resistance gene against a plant virus, bacterium, fungus, nematode or other pathogen;
 - a plant virus resistance gene that confers resistance against a virus selected from the group consisting of: alfalfa mosaic virus, subterranean clover stunt virus, subterranean clover mottle virus, subterranean clover red leaf virus, potato leafroll virus, tomato spotted wilt virus, bean yellow mosaic virus, white clover mosaic virus, clover yellow vein virus, potato virus X (PVX), potato virus Y (PVY) potato virus S (PVS), potato virus M (PVM) potato virus A (PVA), cucumber mosaic virus, rice ragged stunt virus and barley yellow dwarf virus;
 - a gene to improve nutritional value of plants including sunflower high sulphur gene SF8;
 - a bloat resistance gene;
 - an antibody gene;
 - a cereal thionin and ribosome inactivating protein gene;
 - an insect resistance gene including BT toxin gene and proteinase inhibitor gene obtained from *Nicotiana glauca*;
 - a selectable marker gene that confers resistance against kanamycin, phosphinothricin, spectinomycin or hygromycin;

- a reporter gene including GUS, CAT and pigment genes; and
 - a gene encoding a regulatory protein which modulates expression of a gene in plant cells.
11. A genetic construct comprising an isolated SCSV promoter operable in a plant cell and at least one restriction endonuclease site downstream of said promoter to facilitate insertion of a heterologous gene operably linked to said promoter, wherein said SCSV promoter comprises a nucleotide sequence obtained from the group consisting of:
- SEQ ID NO: 1 or a sequence complementary thereto;
 - SEQ ID NO: 3 or a sequence complementary thereto;
 - SEQ ID NO: 4 or a sequence complementary thereto;
 - SEQ ID NO: 5 or a sequence complementary thereto;
 - SEQ ID NO: 7 or a sequence complementary thereto; and
 - a fragment of any one of (i) to (v), wherein said fragment is operable in a plant cell.
12. The genetic construct according to claim 11 further comprising a termination and/or polyadenylation sequence obtained from SCSV, wherein said termination and/or polyadenylation sequence is located at the 3' end of said heterologous gene when said gene is inserted into said restriction endonuclease site.
13. The genetic construct according to claim 12 wherein said termination and/or polyadenylation sequence is obtained from an SCSV segment selected from the group consisting of: SCSV segment 1 (SEQ ID NO:1); SCSV segment 3 (SEQ ID NO:3); SCSV segment 4 (SEQ ID NO:4); SCSV segment 5 (SEQ ID NO:5); SCSV segment 7 (SEQ ID NO:7); and a transcription termination competent or polyadenylation competent fragment of any one of SEQ ID NOS: 1, 3-5 or 7.
14. The genetic construct according to claim 12 wherein said termination and/or polyadenylation sequence is obtained from the *Flaveria bidentis* MeA gene.
15. The genetic construct according to claim 11 or 12 further comprising a heterologous gene selected from the group consisting of:
- a resistance gene against a plant virus, bacterium, fungus, nematode or other pathogen;
 - a plant virus resistance gene that confers resistance against a virus selected from the group consisting of; alfalfa mosaic virus, subterranean clover stunt virus, subterranean clover mottle virus, subterranean clover red leaf virus, potato leafroll virus, tomato spotted wilt virus, bean yellow mosaic virus, white clover mosaic virus, clover yellow vein virus, potato virus X (PVX), potato virus Y (PVY), potato virus S (PVS), potato virus M (PVM) potato virus A (PVA), cucumber mosaic virus, rice ragged stunt virus and barley yellow dwarf virus;
 - a gene to improve nutritional value of plants including sunflower high sulphur gene SF8;
 - a bloat resistance gene;
 - an antibody gene;
 - a cereal thionin and ribosome inactivating protein gene;
 - an insect resistance gene including BT toxin gene and proteinase inhibitor gene obtained from *Nicotiana glauca*;
 - a selectable marker gene that confers resistance against kanamycin, phosphinothricin, spectinomycin or hygromycin;
 - a reporter gene including GUS, CAT and pigment genes; and

j) a gene encoding a regulatory protein which modulates expression of a gene in plant cells.

16. A genetic construct comprising at least two heterologous genes, wherein each of said heterologous genes is operably linked to an isolated nanovirus promoter operable in a plant cell, wherein said promoter is obtained from a segment of the subterranean clover stunt virus (SCSV) genome selected from the group consisting of:

- (i) SCSV segment 1 (SEO ID NO: 1);
- (ii) SCSV segment 3 (SEO ID NO: 3);
- (iii) SCSV segment 4 (SEO ID NO: 4);
- (iv) SCSV segment 5 (SEO ID NO: 5);
- (v) SCSV segment 7 (SEO ID NO: 7);
- (vi) a nucleotide sequence complementary to any one of (i) to (v); and
- (vii) a fragment of any one of (i) to (vi) which is operable in a plant cell.

17. The genetic construct according to claim 16 comprising at least two different SCSV promoters.

18. The genetic construct according to claim 16 wherein the promoters operably linked to said heterologous genes are the same.

19. The genetic construct according to claim 16 wherein each of said heterologous genes is operably linked to a termination and/or polyadenylation sequence.

20. The genetic construct according to claim 19 wherein the termination and/or polyadenylation sequences linked to said heterologous genes are the same.

21. The genetic construct according to claim 19 wherein the termination and/or polyadenylation sequences linked to said heterologous genes are different.

22. The genetic construct according to claim 19 wherein at least one termination and/or polyadenylation sequence is obtained from an SCSV segment selected from the group consisting of SCSV segment 1 (SEQ ID NO:1); SCSV segment 3 (SEQ ID NO:3); SCSV segment 4 (SEQ ID NO:4); SCSV segment 5 (SEQ ID NO:5); SCSV segment 7 (SEQ ID NO:7); and a transcription termination competent or polyadenylation competent fragment of any one of SEQ ID NOS: 1, 3-5 or 7.

23. The genetic construct according to claim 19 wherein at least one termination and/or polyadenylation sequence is obtained from the MEA gene of *Flaveria bidentris*.

24. The genetic construct according to claim 16 wherein said heterologous genes are selected from the group consisting of:

- a) a resistance gene against a plant virus, bacterium, fungus, nematode or other pathogen;
- b) a plant virus resistance gene that confers resistance against a virus selected from the group consisting of: alfalfa mosaic virus, subterranean clover stunt virus, subterranean clover mottle virus, subterranean clover red leaf virus, potato leafroll virus, tomato spotted wilt virus, bean yellow mosaic virus, white clover mosaic virus, clover yellow vein virus, potato virus X (PVX), potato virus Y (PVY), potato virus S (PVS), potato virus M (PVM), potato virus A (PVA), cucumber mosaic virus, rice ragged stunt virus and barley yellow dwarf virus;
- c) a gene to improve nutritional value of plants including sunflower high sulphur gene SF8;
- d) a bloat resistance gene;
- e) an antibody gene;
- f) a cereal thionin and ribosome inactivating protein gene;
- g) an insect resistance gene including BT toxin gene and proteinase inhibitor gene obtained from *Nicotiana glauca*;

h) a selectable marker gene that confers resistance against kanamycin, phosphinothricin, spectinomycin or hygromycin;

i) a reporter gene including GUS, CAT and pigment genes; and

j) a gene encoding a regulatory protein which modulates expression of a gene in plant cells.

25. A method of expressing a foreign gene in a plant cell said method comprising introducing into said plant cell the genetic construct according to claim 11 wherein a foreign gene is operably linked to the promoter on said genetic construct.

26. The method according to claim 25 wherein the foreign gene is selected from the group consisting of:

- a) a resistance gene against a plant virus, bacterium, fungus, nematode or other pathogen;
- b) a plant virus resistance gene that confers resistance against a virus selected from the group consisting of: alfalfa mosaic virus, subterranean clover stunt virus, subterranean clover mottle virus, subterranean clover red leaf virus, potato leafroll virus, tomato spotted wilt virus, bean yellow mosaic virus, white clover mosaic virus, clover yellow vein virus, potato virus X (PVX), potato virus Y (PVY), potato virus S (PVS), potato virus M (PVM), potato virus A (PVA), cucumber mosaic virus, rice ragged stunt virus and barley yellow dwarf virus;
- c) a gene to improve nutritional value of plants including sunflower high sulphur gene SF8;
- d) a bloat resistance gene;
- e) an antibody gene;
- f) a cereal thionin and ribosome inactivating protein gene;
- g) an insect resistance gene including BT toxin gene and proteinase inhibitor gene obtained from *Nicotiana glauca*;
- h) a selectable marker gene that confers resistance against kanamycin, phosphinothricin, spectinomycin or hygromycin;

i) a reporter gene including GUS, CAT and pigment genes; and

j) a gene encoding a regulatory protein which modulates expression of a gene in plant cells.

27. A method of expressing at least two foreign genes in a plant cell, said method comprising introducing into said plant cell the genetic construct according to claim 16.

28. A transgenic plant comprising an SCSV promoter introduced to said plant and a heterologous gene operably linked to said SCSV promoter, wherein said SCSV promoter comprises a nucleotide sequence obtained from the group consisting of:

- (i) SEQ ID NO: 1 or a sequence complementary thereto;
- (ii) SEQ ID NO: 3 or a sequence complementary thereto;
- (iii) SEQ ID NO: 4 or a sequence complementary thereto;
- (iv) SEQ ID NO: 5 or a sequence complementary thereto;
- (v) SEQ ID NO: 7 or a sequence complementary thereto; and
- (vi) a fragment of any one of (i) to (v), wherein said fragment is operable in a plant cell.

29. The transgenic plant according to claim 28 wherein said heterologous gene is selected from the group consisting of:

- a) a resistance gene against a plant virus bacterium, fungus, nematode or other pathogen;
- b) a plant virus resistance gene that confers resistance against a virus selected from the group consisting of:

alfalfa mosaic virus, subterranean clover stunt virus, subterranean clover mottle virus, subterranean clover red leaf virus, potato leafroll virus, tomato spotted wilt virus, bean yellow mosaic virus, white clover mosaic virus, clover yellow vein virus, potato virus X (PVX), potato virus Y (PVY), potato virus S (PVS), potato virus N (PVM), potato virus A (PVA), cucumber mosaic virus, rice ragged stunt virus and barley yellow dwarf virus;

- c) a gene to improve nutritional value of plants including sunflower high sulphur gene SF8;
- d) a bloat resistance gene;
- e) an antibody gene;
- f) a cereal thionin and ribosome inactivating protein gene;
- g) an insect resistance gene including BT toxin gene and proteinase inhibitor gene obtained from *Nicotiana glauca*;
- h) a selectable marker gene that confers resistance against kanamycin, phosphinothricin, spectinomycin or hygromycin;
- i) a reporter gene including GUS, CAT and pigment genes; and
- j) a gene encoding a regulatory protein which modulates expression of a gene in plant cells.

30. The transgenic plant according to claim **28** or **29** wherein said heteroloaous gene is oderably linked to a terminator and/or polyadenylation sequene obtained from SCSV.

31. The transgenic plant according to claim **30** wherein said terminator and/or polyadenylation sequence is obtained from the *Flaveria bidentis* MeA gene.

32. A transgenic plant comprising the genetic construct according to claim **16**.

33. An isolated SCSV promoter sequence obtained from a nucleotide sequence selected from the group consisting of: SCSV segment 1 (SEQ ID NO:1); SCSV segment 3 (SEQ ID NO:3); SCSV segment 4 (SEQ ID NO:4); SCSV segment 5 (SEQ ID NO:5); SCSV segment 7 (SEQ ID NO:7); and a fragment of any one of SEQ ID NOS: 1, 3-5 or 7.

34. An isolated transcription terminator sequence of SCSV obtained from a nucleotide sequence selected from the group consisting of SCSV segment 1 (SEQ ID NO:1); SCSV segment 3 (SEQ ID NO:3); SCSV segment 4 (SEQ ID NO:4); SCSV segment 5 (SEQ ID NO:5); SCSV segment 7 (SEQ ID NO:7); and a transcription termination competent or polyadenylation competent fragment of any one of SEQ ID NOS: 1, 3-5 or 7.

35. The genetic construct of claim **6** wherein the termination and/or polyadenylation sequence comprises the nucleotide sequence as set forth in SEQ ID NO:8 or a transcription termination competent or polyadenylation competent fragment thereof.

36. The genetic construct of claim **14** wherein the termination and/or polyadenylation sequence comprises the nucleotide sequence as set forth in SEQ ID NO:8 or a transcription termination competent or polyadenylation competent fragment thereof.

37. The genetic construct of claim **23** wherein the termination and/or polyadenylation sequence comprises the nucleotide sequence as set forth in SEQ ID NO:8 or a transcription termination competent or polyadenylation competent fragment thereof.

38. The transgenic plant of claim **31** wherein the termination and/or polyadenylation sequence comprises the nucleotide sequence as set forth in SEQ ID NO:8 or a transcription termination competent or polyadenylation competent fragment thereof.

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